

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:27:40 ; Search time 16.2364 Seconds
(without alignments)
675.565 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	479.5	78.7	116	2	S37456	Ig mu chain - huma
2	476.5	78.2	135	2	S78051	Ig heavy chain pre
3	475.5	78.1	128	2	S31514	Ig heavy chain - h
4	465	76.4	122	2	S69912	Ig V-D-J region (N
5	464.5	76.3	147	2	S13519	Ig heavy chain v r
6	460	75.5	130	2	S30534	Ig heavy chain v r
7	458.5	75.3	140	2	I37782	Ig variable region
8	453	74.4	99	2	S26801	Ig heavy chain v r
9	452.5	74.3	146	2	S09710	Ig heavy chain v r
10	451.5	74.1	121	2	S44113	Ig heavy chain v r
11	451.5	74.1	130	2	S31690	Ig heavy chain v r
12	450.5	74.0	127	2	S39668	Ig heavy chain v r
13	450.5	74.0	146	2	S09711	Ig heavy chain v r
14	449.5	73.8	155	2	S31511	Ig heavy chain - h
15	446.5	73.3	155	2	S31512	Ig heavy chain - h
16	444	72.9	137	2	S31676	Ig heavy chain v r
17	440	72.2	139	2	S31586	Ig heavy chain v r
18	439	72.1	145	2	S78055	Ig heavy chain pre
19	436	71.6	99	2	S26803	Ig heavy chain v r
20	435.5	71.5	123	2	S30530	Ig heavy chain v r
21	434	71.3	129	2	S44114	Ig heavy chain v r
22	433.5	71.2	117	2	S34964	Ig heavy chain pre
23	432.5	71.0	109	2	PH1673	Ig heavy chain v r
24	431	70.8	99	2	S26802	Ig heavy chain v r
25	430	70.6	97	2	PL0118	Ig heavy chain v-I
26	430	70.6	99	2	S26899	Ig heavy chain v r
27	427	70.1	110	2	S44110	Ig heavy chain v-D
28	426	70.0	139	2	A41287	Ig heavy chain pre
29	425.5	69.9	121	2	C55257	Ig gamma heavy cha

RESULT 1

S37456

Ig mu chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37456

R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.

submitted to the EMBL Data Library, September 1993

A;Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from I

A;Reference number: S37453

A;Accession: S37456

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-116 <MCI>

A;Cross-references: UNIPARC:UPI00001161C0; EMBL:X75024; NID:G404313; PIDN:CAAS2932.1; PII

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 479.5; DB 2; Length 116;

Best Local Similarity 76.1%; Pred. No. 7e-38; 5; Indels 9; Gaps 2;

Matches 89; Conservative 14; Mismatches 5; Indels 9; Gaps 2;

Qy 6 GLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYVNSLSKRI 65

Db 1 GLVKPQTLSLCTCTVSGSISGGYWSWIRQHPGKLEWIGYIYSGSTYVNSLSKRV 60

Qy 66 AMSVDTSENKPSLRINSVTAADTAATVYTCARLDGYT-----LDIWQGLTVTVSS 114

Db 61 TISVDTSKNPFSLKLSSTVTAADTAATVYTCAR-GGYSYGYIYVMDVMGKGTTVTVSS 116

RESULT 2

S78051

Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C;Accession: S78051; S23716

R;Harindranath, N.

submitted to the EMBL Data Library, August 1990

A;Reference number: S78051

A;Accession: S78051

A;Molecule type: mRNA

A;Residues: 1-135 <HAR>

A;Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:G37814; PIDN:CAA38306.1; PID:

R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockins,

Int. Immunol. 3, 865-875, 1991

A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h

patient.

A;Reference number: S23716; MUID:92031262; PMID:1718404

A;Accession: S23716

A;Molecule type: mRNA

Qy 110 VTVSS 114
Db 126 VTVSS 130

RESULT 7

Ig variable region (VDJ) (clone T23-9) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C/Accession: I37782; S25476
R/Demason, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A/Title: Somatic diversification in the heavy chain variable region genes expressed by B
A/Reference number: A36876; MUID:94119917; PMID:8290556
A/Accession: I37782
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140 <RES>
A/Cross-references: UNIPARC:UPI0000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID
A/Superfamily: immunoglobulin V region; immunoglobulin homology
F/46-128/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 458.5; DB 2; Length 140;
Best Local Similarity 75.4%; Pred. No. 7.9e-36;
Matches 89; Conservative 12; Mismatches 10; Indels 7; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 25 ESGPGLVKPSETLSLTCTVSGGSISS--YYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 82

Qy 62 KSRITMSVDTSENKPSRLNSVTAADTAVYYCARLD-----GYTLDIWGQGLTVTVSS 114
Db 83 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHNSSSWYGRFYDWGQGLTVTVSS 140

RESULT 8

Ig heavy chain V region (DP-65) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C/Accession: S26801; S26900
R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A/Reference number: S26800; MUID:92201299; PMID:1348029
A/Accession: S26801
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-99 <WEN>
A/Cross-references: UNIPARC:UPI0000116419; EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26900
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-99 <TOM>
A/Cross-references: UNIPARC:UPI0000116419; EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 453; DB 2; Length 99;
Best Local Similarity 86.2%; Pred. No. 1.8e-35;
Matches 81; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 65

Qy 62 KSRITMSVDTSENKPSRLNSVTAADTAVYYCAR 95
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR 99

RESULT 9

Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S09710
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A/Reference number: S09710; MUID:90262535; PMID:2111699
A/Accession: S09710
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-146 <HUG>
A/Cross-references: UNIPARC:UPI0000115E6C; GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 452.5; DB 2; Length 146;
Best Local Similarity 68.3%; Pred. No. 3e-35;
Matches 84; Conservative 16; Mismatches 12; Indels 11; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 25 ESGPGLVKPSETLSLTCTVSGGSISS--YYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 84

Qy 62 KSRITMSVDTSENKPSRLNSVTAADTAVYYCARLDGY-----TLDIWQGGTLTV 111
Db 85 KSRVTISVDTLKNFSLKLSVTAADTAVYYCTR-PCYGDTSVKRVNNDLWQGGTTVT 143

Qy 112 VSS 114
Db 144 VSS 146

RESULT 10

Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C/Accession: S44113
R/Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A/Reference number: S44105
A/Accession: S44113
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-121 <HAW>
A/Cross-references: UNIPARC:UPI000011662F; EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 121;
Best Local Similarity 73.3%; Pred. No. 3e-35;
Matches 85; Conservative 13; Mismatches 15; Indels 3; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYYSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGYISSSSYYWGWTRQPPGKLEWIGSYISGSGTYNNPSL 65

Qy 62 KSRITMSVDTSENKPSRLNSVTAADTAVYYCARLDG--YT-LDIWGQGLTVTVSS 114
Db 66 KSRVTLSVDTSKNQFSLKLSVTAADTGVYICSLSGGYISDFDYSQGLTVTVSS 121

RESULT 11

S31690
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: UNIPARC:UPI0000116471; EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 130;
Best Local Similarity 72.1%; Pred. No. 3.3e-35;
Matches 88; Conservative 11; Mismatches 12; Indels 11; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRHPGKLEWIGYVHSGNTYNPSSL 61
DB 11 ESGPGLVKPSETLSLCTVSGGSISS--YWSWSRQPPGKLEWIGYVHSGNTYNPSSL 68
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCARLDG-----YTLDIWGQGLTAVTV 112
DB 69 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARGSSVLLWFGELLYFYDYWGQGLTAVTV 128

QY 113 SS 114
DB 129 SS 130

RESULT 12

S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C;Accession: S19668; S24445
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19668
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: UNIPARC:UPI0000176C7F; EMBL:X61648
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24445
A;Molecule type: mRNA
A;Residues: 1-118; 'E', 120-121, 'T', 123-126, 'F' <JON>
A;Cross-references: UNIPARC:UPI0000115FE7; EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 127;
Best Local Similarity 69.7%; Pred. No. 3.9e-35;
Matches 85; Conservative 15; Mismatches 13; Indels 9; Gaps 1;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRHPGKLEWIGYVHSGNTYNPSSL 61
DB 6 QSGSGLVKPQTLSLCTVSGGSDSISSGGYSWSWIRQPSGKLEWIGSVHSGNTYNPSSL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCARLDG-----YTLDIWGQGLTAVTV 112
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARGGSTWRSRSLYKHYMDVWGKGLTAVTV 125

QY 113 SS 114
DB 126 SS 127

RESULT 13

S09711
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: UNIPARC:UPI0000176CD3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 146;
Best Local Similarity 68.0%; Pred. No. 4.6e-35;
Matches 83; Conservative 17; Mismatches 13; Indels 9; Gaps 1;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRHPGKLEWIGYVHSGNTYNPSSL 61
DB 25 ESGPGLVKPSETLSVCTVSGGSSGLYWSWIRQPPGKPEWIGYVHSGNTYNPSSL 84
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCARL-----DCYTLDIWGQGLTAVTV 112
DB 85 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARVLVSRTSISQSYMDVWGKGLTAVTV 144

QY 113 SS 114
DB 145 SS 146

RESULT 14

S31511
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoan
A;Reference number: S31509
A;Accession: S31511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 449.5; DB 2; Length 155;
Best Local Similarity 70.8%; Pred. No. 6.1e-35;
Matches 85; Conservative 15; Mismatches 11; Indels 9; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRHPGKLEWIGYVHSGNTYNPSSL 61
DB 38 ESGPGLVKPSETLSLCTVSGGSISS--YWSWSRQPPGKLEWIGYVHSGNTYNPSSL 95
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCAR-----LDGYTLDIWGQGLTAVTV 114
DB 96 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARGGGISWSYDYGMVWGQGLTAVTV 155

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:37 ; Search time 96.3818 Seconds
(without alignments)
834.496 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LSSGGLVKAQTLSLCAV.....RLDGYTLDIWGQTLTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

! Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	483.5	79.4	476	2	Q6GMX1_HUMAN	Q6GMX1 homo sapien
2	473	77.7	478	2	Q72379_HUMAN	Q72379 homo sapien
3	451	74.1	150	2	Q95973_HUMAN	Q95973 homo sapien
4	449	73.7	477	2	Q6GMX7_HUMAN	Q6GMX7 homo sapien
5	446.5	73.3	119	2	Q9UL73_HUMAN	Q9UL73 homo sapien
6	444	72.9	465	2	Q6GMX6_HUMAN	Q6GMX6 homo sapien
7	440	72.2	576	2	Q6P418_HUMAN	Q6P418 homo sapien
8	432	70.9	496	2	Q96KX8_HUMAN	Q96KX8 homo sapien
9	430.5	70.7	492	2	Q72374_HUMAN	Q72374 homo sapien
10	430	70.6	620	2	Q96EY0_HUMAN	Q96EY0 homo sapien
11	419.5	68.9	129	1	HV2F_HUMAN	P01824 homo sapien
12	412.5	67.7	478	2	Q6NYH3_HUMAN	Q6NYH3 homo sapien
13	409.5	67.2	595	2	Q8WUX4_HUMAN	Q8WUX4 homo sapien
14	409.5	67.2	597	2	Q8BU10_HUMAN	Q8BU10 homo sapien
15	409.5	67.2	597	2	Q8GMX5_HUMAN	Q8GMX5 homo sapien
16	409.5	67.2	625	2	Q96AA6_HUMAN	Q96AA6 homo sapien
17	408	67.0	139	2	Q86SX2_HUMAN	Q86SX2 homo sapien
18	405.5	66.6	597	2	Q9BQB8_HUMAN	Q9BQB8 homo sapien
19	405	66.5	130	2	Q91ZD7_HUMAN	Q91ZD7 homo sapien
20	405	66.5	146	1	HV2I_HUMAN	P06331 homo sapien
21	389	63.9	483	2	Q5U413_MOUSE	Q5U413 mus musculus
22	388	63.7	473	2	Q8TC63_HUMAN	Q8TC63 homo sapien
23	383	62.9	136	2	Q6LBQ5_MOUSE	Q6LBQ5 mus musculus
24	378.5	62.2	615	2	Q569B6_RAT	Q569B6 rattus norv
25	377.5	62.0	479	2	Q99M22_MOUSE	Q99M22 mus musculus
26	374.5	61.5	137	1	HV46_MOUSE	P01822 mus musculus
27	374	61.4	116	2	Q72376_HUMAN	Q72376 homo sapien
28	372.5	61.2	119	2	Q53VR3_MOUSE	Q53VR3 mus musculus
29	370.5	60.8	115	2	Q53VQ1_MOUSE	Q53VQ1 mus musculus
30	370.5	60.8	262	2	Q65Z11_MOUSE	Q65Z11 mus musculus
31	369.5	60.7	117	1	HV2G_HUMAN	P01825 homo sapien

32	366.5	60.2	590	2	Q569B8_RAT	Q569b8 rattus norv
33	364.5	59.9	119	2	Q53VQ5_MOUSE	Q53vq5 mus musculus
34	362	59.4	120	2	Q53VR7_MOUSE	Q53vr7 mus musculus
35	362	59.4	122	2	Q9UL75_HUMAN	Q9ul75 homo sapien
36	361.5	59.4	113	1	HV47_MOUSE	P01823 mus musculus
37	357.5	58.7	476	2	Q6MZK7_HUMAN	Q6mzx7 homo sapien
38	353.5	58.0	119	2	Q53VQ9_MOUSE	Q53vr2 mus musculus
39	352.5	57.9	98	2	Q53VR2_MOUSE	Q53vr2 mus musculus
40	349.5	57.4	477	2	Q510J1_RAT	Q510j1 rattus norv
41	342.5	56.2	116	1	HV61_MOUSE	P18532 mus musculus
42	341.5	56.1	116	1	HV60_MOUSE	P18531 mus musculus
43	338.5	55.6	98	2	Q53VQ4_MOUSE	Q53vq4 mus musculus
44	334.5	54.9	98	2	Q53VQ8_MOUSE	Q53vq8 mus musculus
45	334	54.8	117	1	HV62_MOUSE	P18533 mus musculus

ALIGNMENTS

RESULT 1
Q6GMX1_HUMAN
ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1, 2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MDL=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC073773; AAH73773.1; -, mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

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DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DD89D CRC64;

Query Match 79.4%; Score 483.5; DB 2; Length 476;
Best Local Similarity 72.6%; Pred. No. 1.2e-41;
Matches 90; Conservative 16; Mismatches 5; Indels 13; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSIRQHPGKLEWIGYIYHSGTYNPSL 61
Db 25 ESGPGLVKPQTLSLTCTVSGSISGDDYWSIRQHPGKLEWIGYIYHSGTYNPSL 84
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYFCARGLDGYTLDIWGQGLTVTVSS 110
Db 85 KSRVTISLDTSKNQFSLKNSVTAADTAVYFCARGLDGYTLDIWGQGLTVTVSS 142
QY 111 TVSS 114
Db 143 TVSS 146

RESULT 2
Q72379 HUMAN
ID Q72379_HUMAN PRELIMINARY; PRT; 478 AA.
AC Q72379
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFp686K04218
GN Names:DKFp686K04218;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
Behcet's patient with arthritis.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Harindranath N., Goldfarb I.S., Ikematsu H., Burastero S.E.,
Wildner R.L., Notkins A.L., Casali P.;
RT "Complete sequence of the genes encoding the VH and VL regions of low-
and high-affinity monoclonal IGM and IgA1 rheumatoid factors produced
by CD5+ B cells from a rheumatoid arthritis patient.";
RL Int. Immunol. 3:865-875(1991).
DR EMBL; AF103795; AAC79084.1; -; mRNA.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; IG7J.
DR SMR; O95973; 20-147.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL. 1 19 Potential.
FT CHAIN. 20 >150 VH4 heavy chain variable region.
FT NON_TER. 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04939AA7C9 CRC64;

Query Match 74.1%; Score 451; DB 2; Length 150;
Best Local Similarity 74.3%; Pred. No. 8.2e-39;
Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSIRQHPGKLEWIGYIYHSGTYNPSL 61
Db 25 ESGPGLVKPSETLSLCTVSGSISSTNYWGWIRQHPGKLEWIGSLHNSGSDYNNPSL 84
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYFCARGLDGYTLDIWGQGLTVTVSS 114
Db 85 KSRVTISLDTSKNQFSLKNSVTAADTAVYFCARGLDGYTLDIWGQGLTVTVSS 137

RESULT 4
Q6GMX7 HUMAN
ID Q6GMX7_HUMAN PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strauberg R.J.
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073765; AAH73765.1; -; mRNA.
DR SMR; O6GMX7; 247-455.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;
Query Match 73.7%; Score 449; DB 2; Length 477;
Best Local Similarity 75.7%; Pred. No. 4.8e-38;
Matches 87; Conservative 10; Mismatches 14; Indels 4; Gaps 2;
Qy 2 ESGGLVKPAQTLSLSCAVSGSRSQGYWWSWIRQHPGKLEWIGYIYHSGNTYTPSL 61
Db 25 ESGGLVKPSETLSLTCTVSGGSIS--YWSWIRQTAGKLEWIGYIYHSGNTYTPSL 82
Qy 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG--YTLDIWGGTGLVTSS 114
Db 83 KSRVTLSDTSKQFSLKLSLTAAADTAVYVCARLSNWGPYFDYWGQGLVTSS 137
RESULT 5
Q9UL73_HUMAN
ID Q9UL73_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RT J. Exp. Med. 174:1639-1652(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2511001;
RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
RT "The smaller human VH gene families display remarkably little
RT polymorphism.";
RL EMBL; AF035041; AAD56277.1; -; mRNA.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; IG7J.
DR SMR; Q9UL73; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 119
FT SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;
Query Match 73.3%; Score 446.5; DB 2; Length 119;
Best Local Similarity 74.1%; Pred. No. 1.9e-39;
Matches 86; Conservative 12; Mismatches 13; Indels 5; Gaps 2;
Qy 2 ESGGLVKPAQTLSLSCAVSGSRSQGYWWSWIRQHPGKLEWIGYIYHSGNTYTPSL 61
Db 6 ESGGLVKPSETLSLTCTVSGGSIS--YWSWIRQHPGKLEWIGYIYHSGNTYTPSL 63
Qy 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG--YTLDIWGGTGLVTSS 114
Db 64 KSRVTLSDTSKQFSLKLSLTAAADTAVYFCARLSNWGPYFDYWGQGLVTSS 119
RESULT 6
Q6GMX6_HUMAN
ID Q6GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_1.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FD81386E CRC64;

Query Match 72.9%; Score 444; DB 2; Length 465;
Best Local Similarity 77.0%; Pred. No. 1.5e-37;
Matches 87; Conservative 9; Mismatches 15; Indels 2; Gaps 1;

QY 2 ESGPGLVKPQATLSLCAVSGGSTRSGGYVWSWIRQHPGKLEWIGVYHSGNTYNP 61
DB 25 ESGPGLVKPSETLSLTCTVSGGSI--SGYVWSWIRQHPGKLEWIGRIYTS 82
QY 62 KSIAMSVDTSENKFSRLNSVTAADTAVYVCARLDGTYLDINGQGTLT 114
DB 83 KSRVTSVDTSKNQFSLKLSVTAADTAVYVCARGTFYDYNGQGTLT 135

RESULT 7
Q6P418 HUMAN
ID Q6P418 HUMAN PRELIMINARY; PRT; 576 AA.
AC Q6P418
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -; mRNA.
DR HSSP; P01820; 1A7N.
DR Ensembl; ENSG00000196122; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 576 AA; 63364 MW; FBB97C949D720F1E CRC64;
Query Match 72.2%; Score 440; DB 2; Length 576;
Best Local Similarity 73.3%; Pred. No. 5.1e-37;
Matches 85; Conservative 13; Mismatches 14; Indels 4; Gaps 2;
QY 2 ESGPGLVKPQATLSLCAVSGGSTRSGGYVWSWIRQHPGKLEWIGVYHSGNTYNP 61
DB 32 ESGPGLVKPSETLSLTCTVSGGSI--SGYVWSWIRQHPGKLEWIGRIYTS 90
QY 62 KSIAMSVDTSENKFSRLNSVTAADTAVYVCARLDG---YTDINGQGTLT 114
DB 91 KSRVTSVDTSKNQFSLKLSVTAADTAVYVCASLDGDIYVYGVMDVWGQGT 146
RESULT 8
Q96KX8 HUMAN
ID Q96KX8 HUMAN PRELIMINARY; PRT; 496 AA.
AC Q96KX8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -; mRNA.
DR HSSP; P01876; IOWO.
DR SMR; Q96KX8; 266-474.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 496 AA; 53392 MW; D346929849040D69 CRC64;
Query Match 70.9%; Score 432; DB 2; Length 496;
Best Local Similarity 65.2%; Pred. No. 2.9e-36;
Matches 83; Conservative 13; Mismatches 16; Indels 8; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGYVWIRQHPGKLEWIGYVHSGNTYNP 61
DB 25 ESGPGLVKSSETLSLTCVSGSISSSSYWGWIRQPPGKLEWIANITYSGITYNP 84
QY 62 KSRIVMSVDTSENKFSRLNLSVTAADTAVYVCARLDGVT-----LDIWQGGTLVT 114
DB 85 KSRVTSISVDTSENKQSLKRLSVTAADTAVYVCAR-HGYSRGRGTAYDWQGGTLVT 143
RESULT 9
Q72374 HUMAN
ID Q72374 HUMAN PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q72374; 262-470.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 70.7%; Score 430.5; DB 2; Length 492;
Best Local Similarity 71.6%; Pred. No. 4.2e-36;
Matches 83; Conservative 13; Mismatches 17; Indels 3; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGYVWIRQHPGKLEWIGYVHSGNTYNP 61
DB 37 ESGPGLVKSSETLSLTCVSGSISSSSYWGWIRQPPGKLEWIANITYSGITYNP 96
QY 62 KSRIVMSVDTSENKFSRLNLSVTAADTAVYVCARLDG--YTLDIWQGGTLVT 114
DB 97 KSRITFVDTSKNHFSLRLSVTAADTAVYVCVRHVEGPGYGFDPGQGGTLVT 152
RESULT 10
Q96EYO HUMAN
ID Q96EYO HUMAN PRELIMINARY; PRT; 620 AA.
AC Q96EYO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=1904154;
RA Neale G.A., Kitchingman G.R.;
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT chain enhancer region contain a non-translatable exon and are
RT extremely heterogeneous at the 5' end.";
RL Nucleic Acids Res. 19:2427-2433 (1991).
DR EMBL; BC011857; AAH11857.2; -; mRNA.
DR PIR; S15590; S15590.
DR HSSP; P01820; 1G7J.
DR SMR; Q96EYO; 27-251.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A46E8FF27B CRC64;

Query Match 70.6%; Score 430; DB 2; Length 620;
Best Local Similarity 74.4%; Pred. No. 6.1e-36;
Matches 87; Conservative

QY 2 ESGPGLVKPAQTLISLSCAVSGGSIIRGGYVWIRQHPGKLEWIGVIYHSGNTYNP 61
DB 32 ESGPGLVKPSETLSLTCTVSGGSISS--YVWIRQHPAGKLEWIGRIYTS 89
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICA---RLDGYTLDIWGQTLTV 114
DB 90 KSRVTSVDTSKNQFSLKLSVTAADTAVYICASQPWELPTVGLFYWGQTLTV 146

RESULT 11
HV2F HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N.; Tetaert D.; Debuire B.; Lin L.-C.; Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
immunoglobulin D."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
CC -I- MISCELLANEOUS: This chain was isolated from an IgD myeloma
protein.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02099; D2HUMA.
CC HSSP; P01820; IG7J.
CC GlycoSuiteDB; P01824; -.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin v region.
FT DOMAIN 1
FT NON TER 129 129 Ig-like.
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47AB851319 CRC64;

Query Match 68.9%; Score 419.5; DB 1; Length 129;
Best Local Similarity 62.7%; Pred. No. 1.3e-35;
Matches 79; Conservative
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QY 2 ESGPGLVKPAQTLISLSCAVSGGSIIRGGYVWIRQHPGKLEWIGVIYHSGNTYNP 61
DB 6 ESGPGLVKPSETLSLTCTVSGGSIIRGGYVWIRQHPGKLEWIGVIYHSGNTYNP 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICAR-----LDGYTLDIWGQ 108
DB 66 RGRVTISVDTSRNQFSLNLSMSAADTAVYICARGNPPPYDYGTSDDG--IDV 123
QY 109 LVTVSS 114
DB 124 TVHVS 129

RESULT 12
Q6NYH3 HUMAN
ID Q6NYH3_HUMAN PRELIMINARY; PRT; 478 AA.
AC Q6NYH3;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Udwin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaby S.J.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahy J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;
RA Schnerch A.; Schein J.E.; Jones S.U.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Blood;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC066594; AAH66594.1; -; mRNA.
DR HSSP; P01820; 1A7N.
DR SMR; Q6NYH3; 248-456.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 51856 MW; 5F8B98F60F077256 CRC64;

Query Match 67.7%; Score 412.5; DB 2; Length 478;
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Best Local Similarity 66.9%; Pred. No. 3e-34;
Matches 79; Conservative 17; Mismatches 13; Indels 9; Gaps 3;

QY 2 ESGPGLVKAQTLISLCAVSGGIRSGYTWIRHQHKGLEWIGYVHSNTYVPSL 61
Db 25 ESGPGLVKAQTLISLCAVSGGIRSGYTWIRHQHKGLEWIGYVHSNTYVPSL 82

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAIVYCARLDGY-----TLDIWGGQGLTVTVSS 114
Db 83 ESRVTMSVDTSENKFSRLNSVTAADTAIVYCARLDGY-----TLDIWGGQGLTVTVSS 138

RESULT 13
Q8WUX4_HUMAN
ID Q8WUX4_HUMAN PRELIMINARY; PRT; 595 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K.B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX NIH MGC Project;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002963; AA02963.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q8WUX4; 27-256.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.

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SMART; SM00407; IGcl; 4.
SMART; SM00408; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65291 MW; 0D4B50776545714E CRC64;

Query Match 67.2%; Score 409.5; DB 2; Length 595;
Best Local Similarity 66.7%; Pred. No. 7.9e-34;
Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVKAQTLISLCAVSGGIRSGYTWIRHQHKGLEWIGYVHSNTYVPSL 63
Db 34 GAGLLKPSSETLSLTCGVYGGSP--SGYVSWIRQPPGKLEWIGVHSNTYVPSL 91

QY 64 RIAMSVDTSENKFSRLNSVTAADTAIVYCARLDGY-----TLDIWGGQGLTVTVSS 114
Db 92 RVTISVDTSENKFSRLNSVTAADTAIVYCARLDGY-----TLDIWGGQGLTVTVSS 151

RESULT 14
Q8BU10_HUMAN
ID Q8BU10_HUMAN PRELIMINARY; PRT; 597 AA.
AC Q8BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K.B., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX NIH MGC Project;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC002963; AA02963.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q8BU10; 20-249.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 1.

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Job time : 96.3818 secs

Job time : 96.3818 sec

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:36:55 ; Search time 24.3545 Seconds
(without alignments)
386.993 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LESGPGLVKPAQTLSLCAV.....RLDGYTLDIWGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501.5	82.3	117	2	US-10-330-613A-13
2	499	81.9	473	2	US-09-049-672A-4
3	496	81.4	172	2	US-09-472-087-7
4	496	81.4	172	2	US-09-472-087-86
5	494.5	81.2	119	2	US-10-330-613A-25
6	489.5	80.4	117	2	US-10-330-613A-5
7	482	79.1	487	2	US-09-800-729-145
8	476.5	78.2	117	2	US-10-330-613A-33
9	472.5	77.6	121	2	US-10-330-613A-37
10	471.5	77.4	119	1	US-08-360-125-5
11	471.5	77.4	119	1	US-08-450-578-5
12	471.5	77.4	119	1	US-09-017-628-5
13	471.5	77.4	119	1	US-09-014-880-5
14	471.5	77.4	119	2	US-09-025-769B-39
15	471.5	77.4	119	2	US-09-025-769B-65
16	471.5	77.4	119	2	US-08-450-363-5
17	471.5	77.4	119	2	US-09-490-070A-39
18	471.5	77.4	119	2	US-09-490-070A-65
19	471.5	77.4	119	2	US-09-490-153-39
20	471.5	77.4	119	2	US-09-490-153-65
21	471.5	77.4	119	2	US-09-467-903-5
22	471.5	77.4	119	2	US-09-490-324-39
23	471.5	77.4	119	2	US-09-490-324-65
24	468	76.8	120	2	US-09-424-840B-20
25	466	76.5	122	1	US-08-360-125-11
26	466	76.5	122	1	US-08-450-578-11
27	466	76.5	122	1	US-09-017-628-11

28	466	76.5	122	1	US-09-014-880-11	Sequence 11, Appl
29	466	76.5	122	2	US-08-450-363-11	Sequence 11, Appl
30	466	76.5	122	2	US-09-467-903-11	Sequence 11, Appl
31	465.5	76.4	117	2	US-09-720-493-2	Sequence 2, Appl
32	455	74.7	118	2	US-09-025-769B-25	Sequence 25, Appl
33	455	74.7	118	2	US-09-490-070A-25	Sequence 25, Appl
34	455	74.7	118	2	US-09-490-153-25	Sequence 25, Appl
35	455	74.7	118	2	US-09-490-324-25	Sequence 25, Appl
36	453	74.4	99	2	US-10-194-975-36	Sequence 36, Appl
37	453	74.4	99	2	US-10-194-975-39	Sequence 39, Appl
38	453	74.4	99	2	US-10-330-613A-45	Sequence 45, Appl
39	453	74.4	99	2	US-10-330-613A-57	Sequence 57, Appl
40	453	74.4	99	2	US-10-330-613A-65	Sequence 65, Appl
41	453	74.4	99	2	US-10-330-613A-73	Sequence 73, Appl
42	453	74.4	99	2	US-10-330-613A-77	Sequence 77, Appl
43	453	74.4	118	2	US-08-545-809A-116	Sequence 116, App
44	453	74.4	118	2	US-09-515-697-116	Sequence 116, App
45	452.5	74.3	121	2	US-10-330-613A-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-330-613A-13
; Sequence 13, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudaa, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match 82.3%; Score 501.5; DB 2; Length 117;
Best Local Similarity 81.4%; Pred. No. 5.6e-44;
Matches 92; Conservative 13; Mismatches 7; Indels 1; Gaps 1;
Qy 2 ESGPGLVKPAQTLSLCAVSGGSISSGGYWTWIRQHPGKLEWIGYVHSGNTYNP 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSISSGGYWTWIRQHPGKLEWIGYVHSGNTYNP 65
Qy 62 KSRTAMSVDTSENKFSURLNSVTAADTAVYYCARLDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-EGDGFYWGQGLTVTVSS 117

RESULT 2
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PP-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTU01
; CLONE: 1513264
;
US-09-049-672A-4

Query Match      81.9%; Score 499; DB 2; Length 473;
Best Local Similarity 78.2%; Pred. No. 5.3e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;

QY  2  ESFGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  25  ESFGLVKPSETLSLTCVAVSGSITSGGYWWSWIRQHPGKLEWIGYIYSGTLYNP 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  62  KSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLD-----GYLDINCOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  85  KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARDVGLRGNGYGMVWGQGLVT 143
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-330-613A-25

Query Match      81.4%; Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY  3  SGFGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  1  SGFGLVKPSQLSLTCTVSGGSISGGHYWWSWIRQHPGKLEWIGYIYIGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  63  SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  61  SRVTISVDTSKNQFSLKLSVTAADTAVVYCARDSDGYTGIDVWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-86

Query Match      81.4%; Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY  3  SGFGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  1  SGFGLVKPSQLSLTCTVSGGSISGGHYWWSWIRQHPGKLEWIGYIYIGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  63  SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  61  SRVTISVDTSKNQFSLKLSVTAADTAVVYCARDSDGYTGIDVWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-10-330-613A-25
; Sequence 25, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-330-613A-25
```

```
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PP-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTU01
; CLONE: 1513264
;
US-09-049-672A-4

Query Match      81.9%; Score 499; DB 2; Length 473;
Best Local Similarity 78.2%; Pred. No. 5.3e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;

QY  2  ESFGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  25  ESFGLVKPSETLSLTCVAVSGSITSGGYWWSWIRQHPGKLEWIGYIYSGTLYNP 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  62  KSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLD-----GYLDINCOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  85  KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARDVGLRGNGYGMVWGQGLVT 143
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-330-613A-25

Query Match      81.4%; Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY  3  SGFGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  1  SGFGLVKPSQLSLTCTVSGGSISGGHYWWSWIRQHPGKLEWIGYIYIGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  63  SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  61  SRVTISVDTSKNQFSLKLSVTAADTAVVYCARDSDGYTGIDVWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-86

Query Match      81.4%; Score 496; DB 2; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY  3  SGFGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  1  SGFGLVKPSQLSLTCTVSGGSISGGHYWWSWIRQHPGKLEWIGYIYIGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  63  SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  61  SRVTISVDTSKNQFSLKLSVTAADTAVVYCARDSDGYTGIDVWGQGLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-10-330-613A-25
; Sequence 25, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-330-613A-25
```


Query Match 81.2%; Score 494.5; DB 2; Length 119;
Best Local Similarity 82.6%; Pred. No. 3e-43; Indels 3; Gaps 2;
Matches 95; Conservative 8; Mismatches 9; Indels 3; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLTLCTVSGSINGGCYWSWIRQHPGKLEWIGYIYSSGTYNNPSL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCARLDGTY--LDWGQGLTVTVSS 114
DB 66 KSRITISVDTSKNQFSLKLSMTAADTAVYVCAR-DRETAGFDYWGQGLTVTVSS 119

RESULT 6
US-10-330-613A-5
; Sequence 5, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR FILING DATE: 2002-12-26
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-5

Query Match 80.4%; Score 489.5; DB 2; Length 117;
Best Local Similarity 81.6%; Pred. No. 9.4e-43; Indels 3; Gaps 2;
Matches 93; Conservative 11; Mismatches 7; Indels 3; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLTLCTVSGSINGGCYWSWIRQHPGKLEWIGYIYSSGTYNNPSL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCAR-LDGYTLDIWGQGLTVTVSS 114
DB 66 KSRITISVDTSKNQFSLKLSMTAADTAVYVCARGGDY--KYWGQGLTVTVSS 117

RESULT 7
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

Query Match 79.1%; Score 482; DB 2; Length 487;
Best Local Similarity 74.8%; Pred. No. 3e-41; Indels 10; Gaps 2;
Matches 92; Conservative 12; Mismatches 9; Indels 10; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
DB 25 ESGPGLVKPSETLSLTCTVSGSINGGCYWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 84
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCAR-----LDGYTL-----DIWGQGLTVT 111
DB 85 KSRITISVDTSONQFSLRLSSVTAADTAVYVCARQKHRAHEDGYQLSYRGFDYWGQGLTVT 144
QY 112 VSS 114
DB 145 VSS 147

RESULT 8
US-10-330-613A-33
; Sequence 33, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-33

Query Match 78.2%; Score 476.5; DB 2; Length 117;
Best Local Similarity 78.9%; Pred. No. 2e-41; Indels 3; Gaps 2;
Matches 90; Conservative 14; Mismatches 7; Indels 3; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
DB 6 QSGPGLVKPSETLSLTCTVSGSINGGCYWSWIRQHPGKLEWIGYIYSSGTYNNPSL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYVCAR-LDGYTLDIWGQGLTVTVSS 114
DB 66 KSRITISVDTSKNQFSLKLSMTAADTAVYVCARGGDYR--YWGQGLTVTVSS 117

RESULT 9
US-10-330-613A-37
; Sequence 37, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-37

Query Match 77.6%; Score 472.5; DB 2; Length 121;
Best Local Similarity 76.3%; Pred. No. 5.4e-41; Indels 7; Gaps 2;
Matches 90; Conservative 13; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSETLSLTCTVSGSIST--YWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 63

QY 62 KSRVSVDTSENKFSRLNSVTAADTAVYCARLDGYTL-----DIWGQGLTVTVSS 114
Db 64 KSRVSVDTSENKFSRLNSVTAADTAVYCARLDGYTL-----DIWGQGLTVTVSS 121

RESULT 10
US-08-360-125-5
; Sequence 5, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:

; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-360-125-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 6.7e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;
QY 2 ESGPGLVKAQTLSCAVSGGSIRSGGYTWSWIRHPGKLEWIGYIYHSGNTYNP 61
Db 6 ESGPGLVKAQTLSCAVSGGSIRSGGYTWSWIRHPGKLEWIGYIYHSGNTYNP 65
QY 62 KSRVSVDTSENKFSRLNSVTAADTAVYCA---RLDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVSVDTSENKFSRLNSVTAADTAVYCA---RLDGYTLDIWGQGLTVTVSS 119

RESULT 11
US-08-450-578-5
; Sequence 5, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 6.7e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSISSCGFYWNWIRQHPGKLEWIGYIYSGSTYNP 65

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICA---RLDGYTLDIWGQGLTVTVSS 114
DB 66 KSRVTISLDTSKQFSLKLSLTAADTAVYICARSTELRG--ADYWGQGLTVTVSS 119

RESULT 14
US-09-025-769B-39
Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-025-769B-39
Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 6.7e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSETLSLCTVSGGSISS--YVSWIRQPPGKLEWIGYIYSGSTYNP 63

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICARDG---YTLDIWGQGLTVTVSS 114
DB 64 KSRVTISVDTSKNQFSLKLSLTAADTAVYICARWGGDGFYAMDYWGQGLTVTVSS 119

RESULT 15
US-09-025-769B-65
Sequence 65, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 6.7e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLISLSCAVSGGSIIRSGGYWIRQHPGKLEWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSETLSLCTVSGGSISS--YVSWIRQPPGKLEWIGYIYSGSTYNP 63

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYICARDG---YTLDIWGQGLTVTVSS 114
DB 64 KSRVTISVDTSKNQFSLKLSLTAADTAVYICARWGGDGFYAMDYWGQGLTVTVSS 119

Search completed: April 3, 2006, 14:40:35
Job time : 25.5545 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 15:10:27 ; Search time 77.9 Seconds
(without alignments)

611,458 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLDIWGQGLTVTVSS 114

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	114	4	US-10-027-725A-7
2	556	91.3	114	4	US-10-027-725A-9
3	546	89.7	114	4	US-10-027-725A-8
4	519	85.2	122	4	US-10-309-762-147
5	518.5	85.1	121	4	US-10-309-762-152
6	517.5	85.0	125	4	US-10-309-762-11
7	514.5	84.5	121	4	US-10-309-762-151
8	512	84.1	118	4	US-10-309-762-138
9	512	84.1	120	4	US-10-309-762-13
10	512	84.1	120	4	US-10-309-762-144
11	509.5	83.7	123	4	US-10-309-762-12
12	509.5	83.7	148	6	US-11-131-648-13
13	509.5	83.7	148	6	US-11-131-648-35
14	508.5	83.5	123	4	US-10-309-762-10
15	508.5	83.5	123	4	US-10-309-762-18
16	508.5	83.5	123	4	US-10-309-762-19
17	508.5	83.5	125	4	US-10-309-762-8
18	508.5	83.5	125	4	US-10-309-762-16
19	508.5	83.5	144	5	US-10-893-576-35
20	506.5	83.2	119	4	US-10-309-762-131
21	505.5	83.0	119	4	US-10-309-762-140
22	505	82.9	252	3	US-09-880-748-1994
23	505	82.9	252	4	US-10-293-418-1994
24	504.5	82.8	125	4	US-10-309-762-153
25	504.5	82.8	480	5	US-10-910-901-6
26	504	82.8	120	4	US-10-309-762-139
27	503.5	82.7	127	4	US-10-309-762-14

28	503	82.6	124	4	US-10-309-762-75	Sequence 75, Appl
29	503	82.6	143	4	US-10-309-762-96	Sequence 96, Appl
30	501.5	82.3	117	4	US-10-330-613-13	Sequence 13, Appl
31	501.5	82.3	117	4	US-10-330-530-13	Sequence 13, Appl
32	501.5	82.3	117	4	US-10-660-357-13	Sequence 13, Appl
33	501	82.3	149	5	US-10-910-901-22	Sequence 22, Appl
34	500.5	82.2	123	5	US-10-893-576-190	Sequence 190, App
35	500.5	82.2	251	4	US-10-120-414-75	Sequence 75, Appl
36	500.5	82.2	251	5	US-10-992-195-75	Sequence 53, Appl
37	500	82.1	125	5	US-10-805-177-53	Sequence 1619, Ap
38	498.5	81.9	253	3	US-09-880-748-1619	Sequence 1619, Ap
39	498.5	81.9	253	4	US-10-293-418-1619	Sequence 31, Appl
40	497.5	81.7	148	5	US-10-893-576-31	Sequence 74, Appl
41	497	81.6	110	4	US-10-309-762-74	Sequence 137, App
42	497	81.6	121	4	US-10-308-817-137	Sequence 137, App
43	497	81.6	121	4	US-10-453-698-137	Sequence 2, Appli
44	497	81.6	128	5	US-10-727-155-2	Sequence 10, Appl
45	497	81.6	128	5	US-10-727-155-10	

ALIGNMENTS

RESULT 1

US-10-027-725A-7

; Sequence 7, Application US/10027725A

; Publication No. US20030082659A1

; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine

; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof

; FILE REFERENCE: 25401-4

; CURRENT APPLICATION NUMBER: US/10/027,725A

; CURRENT FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/259,436

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 7:

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-027-725A-7

Query Match 100.0%; Score 609; DB 4; Length 114;

Best Local Similarity 100.0%; Pred. No. 6e-49;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRHPGKGLWIGYIYHSGNTYNPS 60

Db 1 LESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRHPGKGLWIGYIYHSGNTYNPS 60

Qy 61 LKSRIMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLDIWGQGLTVTVSS 114

Db 61 LKSRIMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLDIWGQGLTVTVSS 114

RESULT 2

US-10-027-725A-9

; Sequence 9, Application US/10027725A

; Publication No. US20030082659A1

; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine

; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof

; FILE REFERENCE: 25401-4

; CURRENT APPLICATION NUMBER: US/10/027,725A

; CURRENT FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/259,436

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 9

; LENGTH: 114

; TYPE: PRT


```
; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match      91.3%; Score 556; DB 4; Length 114;
Best Local Similarity 90.4%; Pred. No. 5.1e-44;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPAQTLISLSCAVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LKSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 114

RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match      89.7%; Score 546; DB 4; Length 114;
Best Local Similarity 89.5%; Pred. No. 4.3e-43;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 LESGPGLVKPAQTLISLSCAVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 LKSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 114

RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match      85.2%; Score 519; DB 4; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.5e-40;
Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

QY 2 ESGPGLVKPAQTLISLSCAVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 122

RESULT 5
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match      85.1%; Score 518.5; DB 4; Length 121;
Best Local Similarity 81.9%; Pred. No. 1.7e-40;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;

QY 2 ESGPGLVKPAQTLISLSCAVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTVSS 121

RESULT 6
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11
```

```
US-10-309-762-138
Query Match      85.0%; Score 517.5; DB 4; Length 125;
Best Local Similarity 81.7%; Pred. No. 2.1e-40;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLTCTVSGGSISGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRIAMSVDTSENKPSLRNSVTAADTAVYYCAR-----LDGY--TLDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARTYYDFLTGPDAPDIWGQGMVTTVSS 125

RESULT 7
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151

Query Match      84.5%; Score 514.5; DB 4; Length 121;
Best Local Similarity 81.0%; Pred. No. 3.9e-40;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLTCTVSGGSISGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRIAMSVDTSENKPSLRNSVTAADTAVYYCARL---DGYTLDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARVLLWFGYGMVWGQGLTVTVSS 121

RESULT 8
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-309-762-138
Query Match      84.1%; Score 512; DB 4; Length 118;
Best Local Similarity 83.2%; Pred. No. 6.5e-40;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLTCTVSGGSISGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRIAMSVDTSENKPSLRNSVTAADTAVYYCARLDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYYSGSDYWGQGLTVTVSS 118

RESULT 9
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      84.1%; Score 512; DB 4; Length 120;
Best Local Similarity 81.9%; Pred. No. 6.6e-40;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLTCTVSGGSISGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRIAMSVDTSENKPSLRNSVTAADTAVYYCARLDGYT---LDIWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR-DGTYWYFGLWGRGLTVTVSS 120

RESULT 10
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
```

```
/ ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      84.1%; Score 512; DB 4; Length 120;
Best Local Similarity 81.9%; Pred. No. 6.6e-40;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYVHSGNTYNPSSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYVHSGNTYNPSSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLDGYYT---LDIWGGGTLVTSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-DGYNWYFDLWGRGTLVTSS 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX-027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-12

Query Match      83.7%; Score 509.5; DB 4; Length 123;
Best Local Similarity 78.8%; Pred. No. 1.2e-39;
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYVHSGNTYNPSSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYVHSGNTYNPSSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARL-----DGYTLDIWGGTTLVTSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARVLLWFGEDYGVDMVGGGTLVTSS 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
US-11-131-648-13
; Sequence 13, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
```

```
/ PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-13

Query Match      83.7%; Score 509.5; DB 6; Length 148;
Best Local Similarity 78.5%; Pred. No. 1.4e-39;
Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYVHSGNTYNPSSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 15 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYVHSGNTYNPSSL 74
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYYCARLDG-----YTLDIWGGTTLVTSS 113
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 KSRVTMSVDTSKNQFSLKLSVTAADTAVYYCAR-DGITWIRGYYGMDVWGGGTLVTSS 133
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 114 S 114
    |
Db 134 S 134

RESULT 13
US-11-131-648-35
; Sequence 35, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-35

Query Match      83.7%; Score 509.5; DB 6; Length 148;
Best Local Similarity 78.5%; Pred. No. 1.4e-39;
```

Matches 95; Conservative 11; Mismatches 6; Indels 9; Gaps 2;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSRSGGYWWSWIRHPGKLEWIGYVHSGNTYNNPSL 61
Db 15 ESGPGLVKPSQTLSTCTVSGGSISSGGYWSWIRHPGKLEWIGYVHSGNTYNNPSL 74
QY 62 KSRVMSVDTSENKFSRLNSVTAADTAATVYVCARL-----YTLDIWGQGLTVTVSS 113
Db 75 KSRVMSVDTSENKFSRLNSVTAADTAATVYVCAR-DGITHIRGYYGMDVWGQGLTVTVSS 133
QY 114 S 114
Db 134 S 134

RESULT 14
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match 83.5%; Score 508.5; DB 4; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.4e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSRSGGYWWSWIRHPGKLEWIGYVHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSISSGGYWSWIRHPGKLEWIGYVHSGNTYNNPSL 65
QY 62 KSRVMSVDTSENKFSRLNSVTAADTAATVYVCARL-----DGYTLDIWGQGLTVTVSS 114
Db 66 KSRVMSVDTSENKFSRLNSVTAADTAATVYVCARAGKYGSGSYLDYWGQGLTVTVSS 123

RESULT 15
US-10-309-762-18
; Sequence 18, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-309-762-18
Query Match 83.5%; Score 508.5; DB 4; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.4e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
QY 2 ESGPGLVKPAQTLSLSCAVSGGSRSGGYWWSWIRHPGKLEWIGYVHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSISSGGYWSWIRHPGKLEWIGYVHSGNTYNNPSL 65
QY 62 KSRVMSVDTSENKFSRLNSVTAADTAATVYVCAR-----LDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVMSVDTSENKFSRLNSVTAADTAATVYVCARVTDYVYGLDVGQGLTVTVSS 123

Search completed: April 3, 2006, 15:20:25
Job time : 78.9 secs

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Db 66 KSRVMSVDTSENKQYSLKLSVTAADTAVVYCARLRPDADYGDYGFYWGQGTMTVTVSS 124

RESULT 2

US-11-266-444-1994
; Sequence 1994, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
; FILE REFERENCE: PF523PID1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1994

Query Match 82.9%; Score 505; DB 7; Length 252;
Best Local Similarity 78.2%; Pred. No. 7.4e-38;
Matches 93; Conservative 12; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSISGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVMSVDTSENKFSRLNSVTAADTAVVYCARL-----DGYTLDIWQOGTLVTVSS 114
Db 66 KSRVMSVDTSENKQYSLKLSVTAADTAVVYCARLRPDADYGDYGFYWGQGTMTVTVSS 124

RESULT 3

US-11-054-515-1619
; Sequence 1619, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1619
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1619

Query Match 81.9%; Score 498.5; DB 7; Length 253;
Best Local Similarity 77.9%; Pred. No. 2.8e-37;
Matches 95; Conservative 12; Mismatches 6; Indels 9; Gaps 3;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSISGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVMSVDTSENKFSRLNSVTAADTAVVYCAR-----LDG--YT--LDIWQOGTLVTV 112
Db 66 KSRVMSVDTSENKQYSLKLSVTAADTAVVYCARSYDILTGRPYTDAFDIWGKGLTVTV 125

QY 113 SS 114
Db 126 SS 127

RESULT 4

US-11-266-444-1619
; Sequence 1619, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
; FILE REFERENCE: PF523PID1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1619
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1619

Query Match 81.9%; Score 498.5; DB 7; Length 253;
Best Local Similarity 77.9%; Pred. No. 2.8e-37;
Matches 95; Conservative 12; Mismatches 6; Indels 9; Gaps 3;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIRSGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSISGGYWWSWIRQHPGKGLEWIGYIYHSGNTYNNPSL 65

QY 62 KSRVMSVDTSENKFSRLNSVTAADTAVVYCAR-----LDG--YT--LDIWQOGTLVTV 112
Db 66 KSRVMSVDTSENKQYSLKLSVTAADTAVVYCARSYDILTGRPYTDAFDIWGKGLTVTV 125

QY 113 SS 114
Db 126 SS 127


```

RESULT 5
US-11-128-900-7
; Sequence 7, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT FILING DATE: 2005-05-12
; CURRENT APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-7

Query Match      81.4%; Score 496; DB 7; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-37;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

Qy 3 SGPGLVKAQTLTSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 62
Db 1 SGPGLVKPSQTLTCTVSGGSISSGGHYWSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 60

Qy 63 SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLTVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARDSGDYGYGIDVWGQGLTVTVSS 114

RESULT 6
US-11-128-900-86
; Sequence 86, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT FILING DATE: 2005-05-12
; CURRENT APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-7

Query Match      81.4%; Score 496; DB 7; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-37;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

Qy 3 SGPGLVKAQTLTSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 62
Db 1 SGPGLVKPSQTLTCTVSGGSISSGGHYWSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 60

Qy 63 SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLTVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARDSGDYGYGIDVWGQGLTVTVSS 114

RESULT 6
US-11-128-900-86
; Sequence 86, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT FILING DATE: 2005-05-12
; CURRENT APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-7

Query Match      81.4%; Score 496; DB 7; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-37;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

Qy 3 SGPGLVKAQTLTSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 62
Db 1 SGPGLVKPSQTLTCTVSGGSISSGGHYWSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 60

Qy 63 SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLTVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARDSGDYGYGIDVWGQGLTVTVSS 114

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; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-86

Query Match      81.4%; Score 496; DB 7; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.2e-37;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

Qy 3 SGPGLVKAQTLTSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 62
Db 1 SGPGLVKPSQTLTCTVSGGSISSGGHYWSWIRQHPGKLEWIGYIYHSGNTYYPNPSLK 60

Qy 63 SRIAMSVDTSENKFSRLNSVTAADTAVVYCARLDG--YTLDIWGQGLTVTVSS 114
Db 61 SRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARDSGDYGYGIDVWGQGLTVTVSS 114

RESULT 7
US-11-054-515-1607
; Sequence 1607, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1607
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1607

Query Match      79.1%; Score 482; DB 7; Length 256;
Best Local Similarity 73.6%; Pred. No. 8.1e-36;
Matches 92; Conservative 10; Mismatches 11; Indels 12; Gaps 1;

Qy 2 ESGPGLVKAQTLTSLSCAVSGSIRSGYYSWIRQHPGKLEWIGYIYHSGNTYYPNPSL 61
Db 6 ESGPGLVKPSQTLTSLTCAVSGGSISSGGYSSWIRQHPGKLEWIGYIYHSGNTYYPNPSL 65

Qy 62 KSRIAMSVDTSENKFSRLNSVTAADTAVVYCARLD-----GYTLDIWGQGLT 109
Db 66 KSRVTISVDRSKNQFSLKLSSTVTAADTAVVYCARQKRGDYDILTGYQLGYAFDIWGRGTP 125

Qy 110 VTVSS 114
Db 126 VTVSS 130

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```
RESULT 8
US-11-266-444-1607
; Sequence 1607, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1607
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1607

Query Match          79.1%; Score 482; DB 7; Length 256;
Best Local Similarity 73.6%; Pred. No. 8.1e-36;
Matches 92; Conservative 10; Mismatches 11; Indels 12; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPKGLWIGYIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGLVKPQTLTSLTCAVSGSISGGSYWSWIRQHPKGLWIGYIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCARL-----GTYLDWGGTL 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDRSKNQFSLKLSVTAADTAVYCARQKRGDYDILTGYQLGYAFD 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 110 VTVSS 114
    |||||
Db 126 VTVSS 130
    |||||

RESULT 9
US-11-054-515-1329
; Sequence 1329, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379

Query Match          79.1%; Score 482; DB 7; Length 256;
Best Local Similarity 73.6%; Pred. No. 8.1e-36;
Matches 92; Conservative 10; Mismatches 11; Indels 12; Gaps 1;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPKGLWIGYIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGLVKPQTLTSLTCAVSGSISGGSYWSWIRQHPKGLWIGYIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCARL-----GTYLDWGGTL 109
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDRSKNQFSLKLSVTAADTAVYCARQKRGDYDILTGYQLGYAFD 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 110 VTVSS 114
    |||||
Db 126 VTVSS 130
    |||||

RESULT 10
US-11-266-444-1329
; Sequence 1329, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; PRIOR FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1329

Query Match          77.8%; Score 474; DB 7; Length 252;
Best Local Similarity 75.2%; Pred. No. 4.1e-35;
Matches 91; Conservative 12; Mismatches 10; Indels 8; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPKGLWIGYIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSETLSLTCTVSGGSISSSSYWGWIRQHPKGLWIGSIYSGSYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCAR-----LDGYTL---DIWGGT 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDRSKNQFSLKLSVTAADTAVYCARQKRGDYDILTGYPLHAFDI 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 114 S 114
    |
Db 126 S 126
    |
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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1329
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1329

Query Match          77.8%; Score 474; DB 7; Length 252;
Best Local Similarity 75.2%; Pred. No. 4.1e-35;
Matches 91; Conservative 12; Mismatches 10; Indels 8; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGSIRSGYYSWIRQHPKGLWIGYIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSETLSLTCTVSGGSISSSSYWGWIRQHPKGLWIGSIYSGSYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRIAMSVDTSENKFSRLNSVTAADTAVYCAR-----LDGYTL---DIWGGT 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRVTISVDRSKNQFSLKLSVTAADTAVYCARQKRGDYDILTGYPLHAFDI 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 114 S 114
    |
Db 126 S 126
    |
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Db 126 S 126

RESULT 11

US-11-054-515-1745

Sequence 1745, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO 1745

LENGTH: 256

TYPE: PRT

ORGANISM: Homo sapiens

US-11-054-515-1745

Query Match 77.8%; Score 474; DB 7; Length 256;

Best Local Similarity 71.4%; Pred. No. 4.1e-35;

Matches 90; Conservative 11; Mismatches 11; Indels 14; Gaps 2;

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWIRQHPGKLEWIGYIYHSGNTYYPNSL 61

Db 6 QSGPGLVKPSETLSLTCTVSGSISGNYWVQHPGKLEWIGYIYDIGNT-YNPSL 64

Qy 62 KSRVMSVDTSENKPSLRNSVTAADTAVYTCARLD-----GYTLDIWGQGT 108

Db 65 KSRVMSVDTSENKPSLRNSVTAADTAVYTCARVPTTYDTSGGYLGEYTYGMDVWGQGT 124

Qy 109 LVTWSS 114

Db 125 LVTWSS 130

RESULT 13

US-10-834-397-39

Sequence 39, Application US/10834397

Publication No. US2006000334A1

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/834,397

FILING DATE: 29-Apr-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

Db 126 S 126

RESULT 11

US-11-054-515-1745

Sequence 1745, Application US/11054515

Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/266,444

CURRENT FILING DATE: 2005-11-04

PRIOR APPLICATION NUMBER: 09/880,746

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

Qy 2 ESGPGLVKPAQTLSLSCAVSGSIRSGGYWIRQHPGKLEWIGYIYHSGNTYYPNSL 61

Db 6 QSGPGLVKPSETLSLTCTVSGSISGNYWVQHPGKLEWIGYIYDIGNT-YNPSL 64

Qy 62 KSRVMSVDTSENKPSLRNSVTAADTAVYTCARLD-----GYTLDIWGQGT 108

Db 65 KSRVMSVDTSENKPSLRNSVTAADTAVYTCARVPTTYDTSGGYLGEYTYGMDVWGQGT 124

Qy 109 LVTWSS 114

Db 125 LVTWSS 130

RESULT 12

US-11-266-444-1745

Sequence 1745, Application US/11266444

Publication No. US20060062789A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato

FILE REFERENCE: PF523P3

CURRENT APPLICATION NUMBER: US/11/266,444

CURRENT FILING DATE: 2005-11-04

PRIOR APPLICATION NUMBER: 09/880,746

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-16

```
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-834-397-39

Query Match 77.4%; Score 471.5; DB 6; Length 119;
Best Local Similarity 77.6%; Pred. No. 3.3e-35;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQHPGKLEWIGYIYSGSTNNPSL 63

QY 62 KSIAMSVDTSENKFSRLNSVTAADTAATVYVCARLDG---YTLDIWGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARWGDDGFYAMDYWGQGLTVTVSS 119

RESULT 14
US-10-834-397-65
; Sequence 65, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappick, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhoun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-834-397-65

Query Match 77.4%; Score 471.5; DB 6; Length 119;
Best Local Similarity 77.6%; Pred. No. 3.3e-35;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQHPGKLEWIGYIYSGSTNNPSL 63

QY 62 KSIAMSVDTSENKFSRLNSVTAADTAATVYVCARLDG---YTLDIWGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAATVYVCARWGDDGFYAMDYWGQGLTVTVSS 119

RESULT 15
US-10-530-171-7
; Sequence 7, Application US/10530171
; Publication No. US20060057147A1
; GENERAL INFORMATION:
; APPLICANT: HIRAKAWA, Youko
; APPLICANT: NIKI, Hisae
; APPLICANT: OIKE, Shinbuke
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: YOSHIYAMA, Yoshiko
; TITLE OF INVENTION: Antibody recognizing antigen
; FILE REFERENCE: 235054
; CURRENT APPLICATION NUMBER: US/10/530,171
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/JP2003/012732
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: JP 2002-291953
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-530-171-7

Query Match 77.4%; Score 471.5; DB 6; Length 119;
Best Local Similarity 75.9%; Pred. No. 3.3e-35;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVKPAQTLSLSCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGGSISSCGFYWWSWIRQHPGKLEWIGYIYSGSTNNPSL 65

QY 62 KSIAMSVDTSENKFSRLNSVTAADTAATVYVCARLDG---RLDGYTLDIWGQGLTVTVSS 114
Db 66 KSRVTISLDTSKNQFSLKLSLTAADTAATVYVCARSTLRG--ADYWGQGLTVTVSS 119

Search completed: April 3, 2006, 15:21:31
Job time : 11.3636 secs
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:09 ; Search time 99.1455 Seconds
(without alignments)
505.209 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1980s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	5	ABG30446 Human IgE
2	608	99.0	114	5	ABG30447 Human IgE
3	546	88.9	114	5	ABG30445 Human IgE
4	514.5	83.8	140	9	Adx98269 Human ant
5	511	83.2	128	8	ADP22124 Human ant
6	511	83.2	128	8	ADP22104 Human ant
7	511	83.2	128	8	ADP22096 Human ant
8	510.5	83.1	121	7	ADP03982 Murine-ex
9	510	83.1	118	7	ADP03968 Murine-ex
10	509.5	83.0	123	7	ADP03870 Murine-ex
11	507.5	82.7	125	7	ADP03871 Murine-ex
12	507	82.6	120	7	ADP03874 Murine-ex
13	507	82.6	120	7	ADP03873 Murine-ex
14	507	82.6	122	7	ADP03977 Murine-ex
15	507	82.6	473	4	AAB36206 Human imm
16	506.5	82.4	119	9	ADX98416 Human ant
17	506	82.4	221	7	ADJ32126 Human int
18	505.5	82.3	121	7	ADP03981 Murine-ex
19	505	82.2	128	8	ADP22120 Human ant
20	504.5	82.2	117	7	ADC99784 Anti-huma
21	504.5	82.2	117	7	ADD05388 Anti-MUC1
22	504.5	82.2	117	7	ADP09826 Human ant
23	503.5	82.0	119	7	ADP03970 Murine-ex
24	502.5	81.8	123	2	Aaw78433 Antibody

25	502.5	81.8	123	5	ABB97976	Abb97976 Heavy cha
26	502.5	81.8	123	7	ADG88414	Adg88414 anti-Ob-R
27	502.5	81.8	123	7	ADP03872	Adp03872 Murine-ex
28	502.5	81.8	144	9	ADX98263	Adx98263 Human ant
29	502	81.8	122	9	AEA21492	Rea21492 Human ant
30	502	81.8	124	7	ADP03935	Adp03935 Murine-ex
31	501	81.6	125	8	ADS16556	Adsl6556 Human ant
32	501	81.6	130	9	ABE01018	Aeb01018 Human IPI
33	501	81.6	252	5	ABP45318	Abp45318 Human BLY
34	501	81.6	252	7	ADG96145	Adg96145 Single ch
35	500.5	81.5	127	4	AAG80217	Aag80217 Human aut
36	500	81.4	120	7	ADP03958	Adp03958 Murine-ex
37	500	81.4	120	7	ADP03969	Adp03969 Murine-ex
38	500	81.4	121	7	ADJ80377	Adj80377 Antibody
39	500	81.4	121	8	ADS16559	Adsl6559 Human ant
40	500	81.4	126	3	AAB30584	Aab30584 A human v
41	500	81.4	126	5	ABP54970	Abp54970 Anti-idio
42	500	81.4	251	5	ABG80712	Abg80712 Amyloid p
43	500	81.4	254	5	ABG80713	Abg80713 Amyloid p
44	500	81.4	263	5	ABG80714	Abg80714 Human IgG
45	499.5	81.4	120	4	AAB62775	Aab62775 Human HIV

ALIGNMENTS

RESULT 1
ABG30446
ID ABG30446 standard; protein; 114 AA.
XX
AC ABG30446;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 60 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX N-PSDB; ABK89638.
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising

PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 37; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergenic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
 CC fab, clone 60 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 100.0%; Score 614; DB 5; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.1e-44;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESGPGVLKPSQTLSTCTCTVSGGSIIRGGYYSWVRQPGKLEWIGNIYHSGNTYNPS 60
 DB 1 LESGPGVLKPSQTLSTCTCTVSGGSIIRGGYYSWVRQPGKLEWIGNIYHSGNTYNPS 60
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSDGYTLDNWGQGLTVVSS 114
 DB 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSDGYTLDNWGQGLTVVSS 114

RESULT 2

ABG30447
 ID ABG30447 standard; protein; 114 AA.

XX AC ABG30447;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 100 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
 KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26
FT Region	/note= "FR1 region"
FT Region	27..33
FT Region	/note= "CDR1 region"
FT Region	34..47
FT Region	/note= "FR2 region"
FT Region	48..63
FT Region	/note= "CDR2 protein"
FT Region	64..95
FT Region	/note= "FR3 region"
FT Region	96..103
FT Region	/note= "CDR2 region"
FT Region	104..114
FT Region	/note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.
 XX (PHAA) PHARMACIA DIAGNOSTICS AB.
 XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.
 XX N-PSDB; ABK89639.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 38; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergenic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
 CC fab, clone 100 heavy chain protein of the invention

XX Sequence 114 AA;

Query Match 99.0%; Score 608; DB 5; Length 114;
 Best Local Similarity 97.4%; Pred. No. 3.7e-44;
 Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGPGVLKPSQTLSTCTCTVSGGSIIRGGYYSWVRQPGKLEWIGNIYHSGNTYNPS 60
 DB 1 LESGPGVLKPSQTLSTCTCTVSGGSIIRGGYYSWVRQPGKLEWIGNIYHSGNTYNPS 60

QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSDGYTLDNWGQGLTVVSS 114
 DB 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYICARSDGYTLDNWGQGLTVVSS 114

RESULT 3

ABG30445

ID ABG30445 standard; protein; 114 AA.

XX AC ABG30445;

XX 21-OCT-2002 (first entry)

XX Human IgE Fab clone 94 heavy chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
 KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26
FT Region	/note= "FR1 region"
FT Region	27..33
FT Region	/note= "CDR1 region"
FT Region	34..47
FT Region	/note= "FR2 region"
FT Region	48..63
FT Region	/note= "CDR2 protein"
FT Region	64..95

```

FT Region /note= "FR3 region"
FT 96..103
FT /note= "CDR2 region"
FT 104..114
FT /note= "FR4 region"
XX WO200253595-A1.
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SR002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
XX N-PSDB; ABK99637.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
XX Disclosure; Page 36; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have anti-allergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX antibodies to Phl p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific fabs of the invention are useful for
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for identification of group 2 allergen-containing pollen and
XX may be used for blocking the binding of grass pollen allergic patients
XX IgE antibodies to Phl p 2. The present sequence represents the human IgG
XX fab, clone 94 heavy chain protein of the invention
XX
XX Sequence 114 AA;
XX
Query Match 88.9%; Score 546; DB 5; Length 114;
Best Local Similarity 89.5%; Pred. No. 7e-39;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
Qy 1 LESGFLVKPSQTLTLCTVSGGSGIRSGGYTWSVWRQPPGKLEWIGNIYHSGNTYVPS 60
Db 1 LESGFLVKPAQTLSLSCAVSGGSGIRSGGYTWSVWRQPPGKLEWIGNIYHSGNTYVPS 60
Qy 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114
Db 61 LKSRITMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLIDWGQGLTVTVSS 114
XX
RESULT 4
ADX98269
ID ADX98269 standard; protein; 140 AA.
XX
XX ADX98269;
XX
XX 05-MAY-2005 (first entry)
XX
XX Human anti-HGF antibody heavy chain variable region protein - SEQ 41.
XX
XX antibody; cytostatic; cancer; neoplasm; solid tumor;
XX hepatocyte growth factor; HGF; light chain variable region.
XX
XX Homo sapiens.

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XX WO2005017107-A2.
XX
XX 24-FEB-2005.
XX
XX 16-JUL-2004; 2004WO-US018936.
XX
XX 18-JUL-2003; 2003US-0489681P.
XX (AMGE-) AMGEN INC.
XX (ABGE-) ABGENIX INC.
XX
XX Burgess TL, Coxon A, Green LL, Zhang K;
XX
XX WPI; 2005-182350/19.
XX N-PSDB; ADX98246.
XX
XX New polypeptide comprising a complementarity determining region (CDR)
XX consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
XX binding hepatocyte growth factor, useful in preparing a composition for
XX treating cancer.
XX
XX Claim 9; SEQ ID NO 41; 301pp; English.
XX
XX The invention relates to a novel isolated polypeptide comprising at least
XX one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
XX or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
XX an antibody heavy or light chain, is capable of binding hepatocyte growth
XX factor (HGF). HGF, also known as scatter factor (SF), has been identified
XX as a potent mitogen for hepatocytes and also as a secretory protein of
XX fibroblasts and smooth muscles that acts to induce motility of epithelial
XX cells. The polypeptide demonstrates cytosolic activity and may be useful
XX in preparing a composition for treating cancer or a solid tumor. The
XX current sequence is that of the human anti-HGF antibody heavy chain
XX variable region protein - SEQ 41 of the invention.
XX
XX Sequence 140 AA;
XX
Query Match 83.8%; Score 514.5; DB 9; Length 140;
Best Local Similarity 84.5%; Pred. No. 4.2e-36;
Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
Qy 2 ESGFGLVKPSQTLTLCTVSGGSGIRSGGYTWSVWRQPPGKLEWIGNIYHSGNTYVPSL 61
Db 25 ESGFGLVKPSQTLTLCTVSGGSGIRSGGYTWSVWRQPPGKLEWIGNIYHSGNTYVPSL 84
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS 114
Db 85 KSRITMSVDTSKNQFSLKLSVTAADTAVVYCARDPYLDYGFDPWGQGLTVTVSS 140
XX
RESULT 5
ADP22124
ID ADP22124 standard; protein; 128 AA.
XX
XX ADP22124;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:30.
XX
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
XX antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
XX neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
XX TNF induced apoptosis; neoplastic disease; breast cancer;
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
XX prostate cancer; immuno-mediated inflammatory disease;
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
XX septic shock; cachexia; anorexia; multiple sclerosis.

```

```
XX OS Homo sapiens.
XX PN WO2004050683-A2.
XX PD 17-JUN-2004.
XX PF 02-DEC-2003; 2003WO-US038281.
XX PP 02-DEC-2002; 2002US-0430729P.
XX PR (ABGE-) ABGENIX INC.
XX PA
XX PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
XX PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX DR WPI; 2004-480601/45.
XX DR N-PSDB; ADP22123.
XX PT New recombinant human monoclonal antibody that specifically binds to
XX PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
XX PT arthritis.
XX PS Example 10; SEQ ID NO 30; 213pp; English.
XX CC
XX CC The present invention describes a human monoclonal antibody (I) that
XX CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
XX CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
XX CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
XX CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX CC (M1) the level of TNFa in a patient sample, comprising contacting with
XX CC (1), and detecting the level of binding between the antibody and TNFa in
XX CC the sample; (2) a composition comprising the antibody or its functional
XX CC fragment and a carrier; (3) treating (M2) an animal suffering from a
XX CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
XX CC animal in need of treatment for the disease by administering the human
XX CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
XX CC apoptosis in an animal by selecting an animal in need of treatment for
XX CC TNFa induced apoptosis by administering the human monoclonal antibody of
XX CC (1). (I) has anabolic, antiarteriosclerotic, antiarthritic,
XX CC antibacterial, antiinflammatory, antipruritic, antirheumatic, eating-
XX CC disorders, immunomodulator, immunosuppressive, nephrotropic,
XX CC multiple sclerosis. The present sequence represents a human anti-TNFA
XX CC antibody heavy chain variable region, which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 128 AA;
XX
XX Query Match 83.2%; Score 511; DB 8; Length 128;
XX Best Local Similarity 78.9%; Pred. No. 7.5e-36;
XX Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
XX
XX QY 2 ESGPGLVKPQTLSLTCTVSGSIRSGGYWVQPPGKGLWIGNIGHGNTYNPSSL 61
XX DB 6 ESGPGLVKPQTLSLTCTVSGSIRSGGYWVQPPGKGLWIGNIGHGNTYNPSSL 65
XX
XX QY 62 KSRITMSVDTSKNHFSLURLSVTAADTAVYCARSDG-----YTLDNWGQGLT 111
XX DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARSDSNQYNWDEVDYGLDVGQGT 125
XX
XX 112 VSS 114
```

Db 126 VSS 128

```
|||
126 VSS 128

RESULT 6
ADP22104
ID ADP22104 standard; protein; 128 AA.
XX
XX ADP22104;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:10.
DE
XX
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipruritic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX Homo sapiens.
OS
XX WO2004050683-A2.
XX PN
XX 17-JUN-2004.
XX PD
XX
XX 02-DEC-2003; 2003WO-US038281.
XX PF
XX 02-DEC-2002; 2002US-0430729P.
XX PR
XX (ABGE-) ABGENIX INC.
XX PA
XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
XX PI Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX DR WPI; 2004-480601/45.
XX DR N-PSDB; ADP22103.
XX
XX New recombinant human monoclonal antibody that specifically binds to
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
XX arthritis.
XX Example 10; SEQ ID NO 10; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (I) that
XX specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
XX (a) a heavy chain complementarity determining region 1 (CDR1) having the
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX (M1) the level of TNFa in a patient sample, comprising contacting with
XX (1), and detecting the level of binding between the antibody and TNFa in
XX the sample; (2) a composition comprising the antibody or its functional
XX fragment and a carrier; (3) treating (M2) an animal suffering from a
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an
XX animal in need of treatment for the disease by administering the human
XX monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
XX apoptosis in an animal by selecting an animal in need of treatment for
XX TNFa induced apoptosis by administering the human monoclonal antibody of
XX (1). (I) has anabolic, antiarteriosclerotic, antiarthritic,
XX antibacterial, antiinflammatory, antipruritic, antirheumatic, eating-
XX disorders, immunomodulator, immunosuppressive, nephrotropic,
XX multiple sclerosis. The present sequence represents a human anti-TNFA
XX antibody heavy chain variable region, which is used in the
XX exemplification of the present invention.
XX Example 10; SEQ ID NO 10; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (I) that
XX specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
XX (a) a heavy chain complementarity determining region 1 (CDR1) having the
XX two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
XX and (b) a light chain CDR1 having the two fully defined 11 amino acid
XX sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
XX (M1) the level of TNFa in a patient sample, comprising contacting with
XX (1), and detecting the level of binding between the antibody and TNFa in
XX the sample; (2) a composition comprising the antibody or its functional
XX fragment and a carrier; (3) treating (M2) an animal suffering from a
XX neoplastic, or an immuno-mediated inflammatory disease by selecting an
XX animal in need of treatment for the disease by administering the human
XX monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
XX apoptosis in an animal by selecting an animal in need of treatment for
XX TNFa induced apoptosis by administering the human monoclonal antibody of
XX (1). (I) has anabolic, antiarteriosclerotic, antiarthritic,
XX antibacterial, antiinflammatory, antipruritic, antirheumatic, eating-
XX disorders, immunomodulator, immunosuppressive, nephrotropic,
XX neuroprotective, vasotropic and antiapoptotic activities, and can be used
XX as a TNFa antagonist. The antibody (I) is useful in the preparation of
```


CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 128 AA;

Query Match 83.2%; Score 511; DB 8; Length 128;
 Best Local Similarity 78.9%; Pred. No. 7.5e-36;
 Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
 QY 2 ESGPGLVKPSQTLTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYSGTYNPSL 61
 Db 6 ESGPGLVKPSQTLTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYSGTYNPSL 65
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTLDNWQGTIVT 111
 Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSDNQYNWDEYDGLDVWQGTIVT 125
 QY 112 VSS 114
 Db 126 VSS 128

RESULT 7

ADP22096
 ID ADP22096 standard; protein; 128 AA.

XX ADP22096;

XX 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:2.

XX human; monoclonal antibody; tumor necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoaric; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.

XX WO2004050683-A2.

XX 17-JUN-2004.

XX 02-DEC-2003; 2003WO-US038281.

XX 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

XX Haak-Frendscho W, Rathanasami P, Pigott C, Liang ML, Lee R;

XX Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX WPI; 2004-480601/45.

XX N-PSDB; ADP22095.

XX New recombinant human monoclonal antibody that specifically binds to

PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.

XX Example 10; SEQ ID NO 2; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumor necrosis factor-alpha (TNFA) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22419) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFA in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFA in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFA induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoaric, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic, and
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.

XX Sequence 128 AA;

Query Match 83.2%; Score 511; DB 8; Length 128;
 Best Local Similarity 78.9%; Pred. No. 7.5e-36;
 Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
 QY 2 ESGPGLVKPSQTLTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYSGTYNPSL 61
 Db 6 ESGPGLVKPSQTLTLCTVSGSIRSGYYSWVRQPGKLEWIGNIYSGTYNPSL 65
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTLDNWQGTIVT 111
 Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSDNQYNWDEYDGLDVWQGTIVT 125
 QY 112 VSS 114
 Db 126 VSS 128

RESULT 8

ADP03982

ID ADP03982 standard; protein; 121 AA.

XX ADP03982;

XX 29-JUL-2004 (first entry)

XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
 DE monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 XX cytosolic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

OS

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XX PN WO2003048328-A2.
XX PD 12-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038550.
XX PR 03-DEC-2001; 2001US-0337275P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Foltz I, Handa M, Gallo M;
XX DR WPI; 2003-523295/49.
XX PS New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX PS Example 2; SEQ ID NO 152; 89pp; English.
XX CC The invention relates to a novel isolated monoclonal antibody (mAb)
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a
XX CC sequence chosen from one of 53 fully defined amino acid sequences given
XX CC in the specification, where the antibody specifically binds carbonic
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX CC tumour or breast cancer, possibly via gene therapy. The current sequence
XX CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX CC (heavy chain variable domain) protein of the invention. The protein was
XX CC generated via the introduction of the human CA IX protein into a
XX CC transgenic mouse strain.
XX SQ Sequence 121 AA;
Query Match 83.1%; Score 510.5; DB 7; Length 121;
Best Local Similarity 82.8%; Pred. No. 7.9e-36;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
QY 2 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWVWVROPKGLGWIGNIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWVWVROPKGLGWIGNIYHSGNTYINPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSD---GYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCAYDILTGAFDIMGQGTMTVTVSS 121
RESULT 9
ADP03968
ID ADP03968 standard; protein; 118 AA.
XX AC ADP03968;
XX DT 29-JUL-2004 (first entry)
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytostatic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX OS Unidentified.
XX PN WO2003048328-A2.
XX PD 12-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038550.
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XX PR 03-DEC-2001; 2001US-0337275P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Foltz I, Handa M, Gallo M;
XX DR WPI; 2003-523295/49.
XX PS New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX PS Example 2; SEQ ID NO 138; 89pp; English.
XX CC The invention relates to a novel isolated monoclonal antibody (mAb)
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a
XX CC sequence chosen from one of 53 fully defined amino acid sequences given
XX CC in the specification, where the antibody specifically binds carbonic
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX CC tumour or breast cancer, possibly via gene therapy. The current sequence
XX CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX CC (heavy chain variable domain) protein of the invention. The protein was
XX CC generated via the introduction of the human CA IX protein into a
XX CC transgenic mouse strain.
XX SQ Sequence 118 AA;
Query Match 83.1%; Score 510; DB 7; Length 118;
Best Local Similarity 85.0%; Pred. No. 8.4e-36;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 2 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWVWVROPKGLGWIGNIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLTLCTVSGGSIRSGGYWVWVROPKGLGWIGNIYHSGNTYINPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSDGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCAYYCARYYSGSDYWGQGLTVTVSS 118
RESULT 10
ADP03870
ID ADP03870 standard; protein; 123 AA.
XX AC ADP03870;
XX DT 29-JUL-2004 (first entry)
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytostatic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX OS Unidentified.
XX PN WO2003048328-A2.
XX PD 12-JUN-2003.
XX PF 02-DEC-2002; 2002WO-US038550.
XX PR 03-DEC-2001; 2001US-0337275P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Foltz I, Handa M, Gallo M;
```

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 10; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX Sequence 123 AA;

SQ

Query Match 83.0%; Score 509.5; DB 7; Length 123;

Best Local Similarity 82.2%; Pred. No. 9.7e-36;

Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVKPSQTLTCTVSGGSIRSGGYWVWVROPKGLWIGNIYHSGNTYYPNPSL 61

DB 6 ESGPGLVKPSQTLTCTVSGGSISGGYWVWVROPKGLWIGNIYHSGNTYYPNPSL 65

QY 62 KSRITMSVDTSKNHFSRLTSTVAADTAVYVCARS-----DGYTLDNMGQGLTVTVSS 114

DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARTYDFTLTGYPDAFDINGQGTMTVTVSS 123

RESULT 11

ADP03871

ID ADP03871 standard; protein; 125 AA.

XX

AC ADP03871;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytostatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX

OS Unidentified.

XX

FN WO2003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPI; 2003-523295/49.

XX

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Claim 1; SEQ ID NO 11; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic

CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention

CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH

CC (heavy chain variable domain) protein of the invention. The protein was

CC generated via the introduction of the human CA IX protein into a

CC transgenic mouse strain.

XX Sequence 125 AA;

SQ

Query Match 82.7%; Score 507.5; DB 7; Length 125;

Best Local Similarity 81.7%; Pred. No. 1.5e-35;

Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLTCTVSGGSIRSGGYWVWVROPKGLWIGNIYHSGNTYYPNPSL 61

DB 6 ESGPGLVKPSQTLTCTVSGGSISGGYWVWVROPKGLWIGNIYHSGNTYYPNPSL 65

QY 62 KSRITMSVDTSKNHFSRLTSTVAADTAVYVCARS-----DGYTLDNMGQGLTVTVSS 114

DB 66 KSRITISVDTSKNQFSLKLSVTAADTAVYVCARTYDFTLTGYPDAFDINGQGTMTVTVSS 125

RESULT 12

ADP03974

ID ADP03974 standard; protein; 120 AA.

XX

AC ADP03974;

XX

DT 29-JUL-2004 (first entry)

XX

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.

XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KW cytostatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial squamous neoplasia;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX

OS Unidentified.

XX

FN WO2003048328-A2.

XX

PD 12-JUN-2003.

XX

PF 02-DEC-2002; 2002WO-US038550.

XX

PR 03-DEC-2001; 2001US-0337275P.

XX

PA (ABGE-) ABGENIX INC.

XX

PI Gudas J, Foltz I, Handa M, Gallo M;

XX

DR WPI; 2003-523295/49.

XX

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 144; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)

CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given

CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

XX Sequence 120 AA;

Query Match 82.6%; Score 507; DB 7; Length 120;
Best Local Similarity 83.6%; Pred. No. 1.5e-35;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
QY 2 ESGPGLVKPSQTLTLCTVSGSIRSGYYWVROPKGLGWIGNIYHSGNTYNPSSL 61
DB 6 ESGPGLVKPSQTLTLCTVSGSIRSGYYWVROPKGLGWIGNIYHSGNTYNPSSL 65
QY 62 KSRITVSDTSKNHFSRLTSVTAADTAVYVCARS DGT---LDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCAR-DGYNWYFDLWGRGLTVTVSS 120

RESULT 13

ADP03873
ID ADP03873 standard; protein; 120 AA.

XX AC ADP03873;
XX DT 29-JUL-2004 (first entry)
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytostatic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX PN WQ2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX PS Claim 1; SEQ ID NO 13; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence

CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

XX Sequence 120 AA;

Query Match 82.6%; Score 507; DB 7; Length 120;
Best Local Similarity 83.6%; Pred. No. 1.5e-35;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
QY 2 ESGPGLVKPSQTLTLCTVSGSIRSGYYWVROPKGLGWIGNIYHSGNTYNPSSL 61
DB 6 ESGPGLVKPSQTLTLCTVSGSIRSGYYWVROPKGLGWIGNIYHSGNTYNPSSL 65
QY 62 KSRITVSDTSKNHFSRLTSVTAADTAVYVCARS DGT---LDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCAR-DGYNWYFDLWGRGLTVTVSS 120

RESULT 14

ADP03977
ID ADP03977 standard; protein; 122 AA.

XX AC ADP03977;
XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytostatic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX Unidentified.

XX PN WQ2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 147; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.

XX Sequence 122 AA;

Query Match 82.6%; Score 507; DB 7; Length 122;
Best Local Similarity 82.1%; Pred. No. 1.6e-35;
Matches 95; Conservative 8; Mismatches 9; Indels 4; Gaps 1;
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWVPPGKLEWIGNIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWVPPGKLEWIGNIYHSGNTYINPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR----SGYTLDNWGGQTLVTSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARYDYDILTGMDVWVGQTLVTSS 122

RESULT 15
AAB36206
ID AAB36206 standard; protein; 473 AA.
XX
AC AAB36206;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-4.
XX
KW Human; immune system associated protein; HISAP-4; immune disorder;
KW infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX
WPI: 2001-030926/04.
DR N-PSDB; AAC66522.
XX
PT New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
PS Claim 1; Col 53-56; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 473 AA;

Query Match 82.6%; Score 507; DB 4; Length 473;
Best Local Similarity 79.8%; Pred. No. 6.5e-35;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWVPPGKLEWIGNIYHSGNTYINPSL 61
DB 25 ESGPGLVKPSETLSLTCAVSGSITSGGYWVWVPPGKLEWIGNIYHSGNTYINPSL 84
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGGQTLVTSS 114
DB 85 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDVGLRGNGYGMVWVGQTLVTSS 143

Search completed: April 3, 2006, 14:27:04
Job time : 100.145 secs

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GenCore version 5.1.7
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QM protein - protein search, using sw model

Run on: April 3, 2006, 14:27:40 ; Search time 16.2364 Seconds
(without alignments)
675.565 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LBSGGLVKPSTLSLTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499.5	81.4	135	2 S78051	Ig heavy chain pre
2	495.5	80.7	147	2 S13519	Ig heavy chain V r
3	487	79.3	130	2 S30534	Ig heavy chain V r
4	480.5	78.3	121	2 S44113	Ig heavy chain V r
5	478.5	77.9	140	2 I37782	Ig variable region
6	477.5	77.8	146	2 S09710	Ig heavy chain V r
7	474.5	77.3	116	2 S37456	Ig mu chain - huma
8	474.5	77.3	130	2 S31690	Ig heavy chain V r
9	474	77.2	122	2 S69912	Ig V-D-J region (N
10	473.5	77.1	128	2 S31514	Ig heavy chain - h
11	472.5	77.0	127	2 S19668	Ig heavy chain V r
12	469	76.4	137	2 S31676	Ig heavy chain V r
13	468.5	76.3	123	2 S30530	Ig heavy chain V r
14	465.5	75.8	155	2 S31511	Ig heavy chain - h
15	463.5	75.5	155	2 S31512	Ig heavy chain - h
16	462	75.2	139	2 S31586	Ig heavy chain V r
17	460.5	75.0	146	2 S09711	Ig heavy chain V r
18	460	74.9	145	2 S78055	Ig heavy chain pre
19	459.5	74.8	109	2 PH1673	Ig heavy chain V r
20	457	74.4	110	2 S44110	Ig heavy chain V-D
21	455	74.1	99	2 S26803	Ig heavy chain V r
22	454	73.9	139	2 A41287	Ig heavy chain pre
23	453	73.8	99	2 S26801	Ig heavy chain V r
24	452	73.6	129	2 S44114	Ig heavy chain V r
25	450	73.3	99	2 S26802	Ig heavy chain V r
26	450	73.3	135	2 S31604	Ig heavy chain V r
27	447	72.8	118	2 S20780	Ig heavy chain V r
28	446	72.6	99	2 S12418	Ig heavy chain V r
29	444.5	72.4	139	2 S31696	Ig heavy chain V r

RESULT 1

S78051

Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C;Accession: S78051; S23716

R;Harindranath, N.

submitted to the EMBL Data Library, August 1990

A;Reference number: S78051

A;Accession: S78051

A;Molecule type: mRNA

A;Residues: 1-135 <HAW>

A;Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:g37814; PIDN:CAA38306.1; PID:

R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins,

Int. Immunol. 3, 865-875, 1991

A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hi

patient.

A;Reference number: S23716; MUID:92031262; PMID:1718404

A;Accession: S23716

A;Molecule type: mRNA

A;Residues: 13-111 <HAW>

A;Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>

F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>

F;27-111/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 81.4%; Score 499.5; DB 2; Length 135;

Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

Qy

2 BSGGLVKPSTLSLTCTVSGSIRSGGYKSWYRQPGKGLWITGNLYHSGNTYVPSL 61

Db

18 BSGGLVKPSTLSLTCTVSGSIRSGGYKSWYRQPGKGLWITGNLYHSGNTYVPSL 77

Qy

62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCAR--SDGYTLDN---WGQGLTVTVSS 114

Db

78 KSRVITISVDTSKNHFSLRLTSVTAADTAVYVCARLGPDPDYTLGDMDVWGQGLTVTVSS 135

RESULT 2

S13519

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S13519

R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked s

A;Reference number: S13519; MUID:91187691; PMID:2011536

A;Accession: S13519

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: UNIPARC:UPI0000115EB5; EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:15-99/Domain: immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 495.5; DB 2; Length 147;
Best Local Similarity 80.2%; Pred. No. 2.7e-37;
Matches 93; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 61
DB 32 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 91

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG---DGYTLDNWGQGLTVTVSS 114
DB 92 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARPILLWFGELFDYWGQGLTVTVSS 147

RESULT 3
S30534
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Marette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30534
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: UNIPARC:UPI0000113F45; EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 487; DB 2; Length 130;
Best Local Similarity 76.0%; Pred. No. 1.3e-36;
Matches 95; Conservative 7; Mismatches 11; Indels 12; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDG-----YTLDNWGQGLT 109
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDKGGFWGYTRNSRAAFDINGQGT 125

QY 110 VTVSS 114
DB 126 VTVSS 130

RESULT 4
S44113
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44113
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A;Reference number: S44105
A;Accession: S44113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <HAW>
A;Cross-references: UNIPARC:UPI000011662F; EMBL:Z31389; NID:g472967; PIDN:CAA83264.1; PID:15-99/Domain: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 480.5; DB 2; Length 121;
Best Local Similarity 78.4%; Pred. No. 4.7e-36;
Matches 91; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGY--TLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARSLSGYISDFYWSQGLTVTVSS 121

RESULT 5
I37782
IG variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
R;Demaision, C.; Chaetagner, P.; There, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: UNIPARC:UPI000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 478.5; DB 2; Length 140;
Best Local Similarity 78.8%; Pred. No. 8.3e-36;
Matches 93; Conservative 9; Mismatches 9; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 61
DB 25 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 82

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGLTVTVSS 114
DB 83 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHNSSSWYGRYFDYWGQGLTVTVSS 140

RESULT 6
S09710
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S09710
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09710
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: UNIPARC:UPI000115B6C; GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g:15-99/Domain: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 146;
Best Local Similarity 73.2%; Pred. No. 1.1e-35;
Matches 90; Conservative 13; Mismatches 9; Indels 11; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 61
DB 25 ESGPGLVKPSQTLSTCTVSGGIRSGYWSVVRPPGKGLWIGNIYHSGNTYNP 84


```
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGY-----TLDNWGQGLTVT 111
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 KSRVTISVDILKNFSLKLSVTAADTAVVYCTR-POGYDTSVRKRVMNMDLWGQGLTVT 143
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 112 VSS 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 VSS 146

RESULT 7
S37456
Ig mu chain - human (fragment)
C:Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human Igm anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
A;Cross-references: UNIPARC:UPI00001161C0; EMBL:X75024; NID:G404313; PIDN:CAA52932.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 474.5; DB 2; Length 116;
Best Local Similarity 77.8%; Pred. No. 1.5e-35;
Matches 91; Conservative 10; Mismatches 7; Indels 9; Gaps 2;

QY 6 GLVPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSLKSRI 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GLVPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSLKSRI 60

QY 66 TMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYT-----LDNWGQGLTVTVSS 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TISVDTSKNQFSLKLSVTAADTAVVYCARG-GYSYGYYYYYYDVMGKGTIVTVSS 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
S31690
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: UNIPARC:UPI0000116471; EMBL:Z14199; NID:G30984; PIDN:CAA78568.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 77.3%; Score 474.5; DB 2; Length 130;
Best Local Similarity 76.2%; Pred. No. 1.7e-35;
Matches 93; Conservative 7; Mismatches 11; Indels 11; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSL 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 ESGPGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSL 68

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTLDNWGQGLTVTV 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSGSVLLWFFGLLYYFDYWGQGLTVTV 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 SS 114
```

```
Db 129 SS 130
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
S69912
Ig V-D-J region (ND) - human
C:Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multipl
A;Reference number: S69909; MUID:94335315; PMID:8057663
A;Accession: S69912
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: UNIPARC:UPI0000116640; EMBL:Z33398; NID:G871347; PIDN:CAA83849.1; PII
A;Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 474; DB 2; Length 122;
Best Local Similarity 76.9%; Pred. No. 1.8e-35;
Matches 90; Conservative 11; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSL 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSL 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----DGYTLDNWGQGLTVTVSS 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRITMSVDTSKNQFSLKLSVTAADTAVVYCARGFFFRGTGYGLTWGQGLTVRLSS 122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
S31514
Ig heavy chain - human
C:Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: UNIPARC:UPI00001160FB; EMBL:X69862; NID:G33086; PIDN:CAA49496.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 128;
Best Local Similarity 77.6%; Pred. No. 2.1e-35;
Matches 90; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSL 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 13 ESGPGLVKPSQTLSTCTVSGSIRSGGYYSWVRQPPGKGLEWIGNIYHSGNTYNNPSL 72
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----SDGYTLDNWGQGLTVTVSS 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 KSRITMSVDTSENOFSLRLTSVTAADTAVVYCARIGYCNFYGFDPGWGQGLTVTVSS 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C:Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
```


A;Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID
C;Superfamily: immunoglobulin V region: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match	75.5%	Score	463.5	DB	2	Length	155
Best Local Similarity	73.3%	Pred. No.	2e-34				
Matches	88	Conservative	12	Mismatches	11	Indels	9
						Gaps	2

Qy	2	ESGPELVKPSQTL	SLTCTVSGGSI	RGCGYYWSVRQPPGKLEWIGNIYHSGNTYYNPSL	61
Db	38	ESGPELVKPSQTL	SLTCTVSGGSI	SS--YYWSWIRQPPGKLEWIGYIYYTGSATYNPPI	95
Qy	62	KSRTMSVDTSKNHFSL	RLTSVTAADTAVYVCARSDG	-----YTLDNWGQGLTVTVSS	114
Db	96	KSRVTISVDTSKNQFSL	KVSSVTAADTAVYVCARGGISSWYVYGMVDVWGQGLTVTVSS		155

Search completed: April 3, 2006, 14:38:06
Job time : 16.2364 secs

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:37 ; Search time 96.3818 seconds.
(without alignments)
834.496 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LBSGCLVKPQSLTCTV.....RSDGYTLDNWGQTLTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	492.5	80.2	476	2	O6GMX1_HUMAN	O6gmx1 homo sapien
2	477	77.7	465	2	O6GMX6_HUMAN	O6gmx6 homo sapien
3	476.5	77.6	492	2	Q7Z374_HUMAN	Q7z374 homo sapien
4	470	76.5	478	2	Q7Z379_HUMAN	Q7z379 homo sapien
5	466	75.9	150	2	O95973_HUMAN	O95973 homo sapien
6	466	75.9	496	2	O96KX8_HUMAN	O96kx8 homo sapien
7	463.5	75.5	119	2	Q9UL73_HUMAN	Q9ul73 homo sapien
8	457	74.4	477	2	O6GMX7_HUMAN	O6gmx7 homo sapien
9	457	74.4	620	2	Q96EY0_HUMAN	Q96ey0 homo sapien
10	451	73.5	576	2	O6P418_HUMAN	Q6p418 homo sapien
11	440.5	71.7	129	1	HV2F_HUMAN	Q81zd7 homo sapien
12	429	69.9	130	2	Q81ZD7_HUMAN	Q81zd7 homo sapien
13	427	69.5	139	2	Q86SX2_HUMAN	O86sx2 homo sapien
14	426.5	69.5	595	2	Q8WUX4_HUMAN	O8wux4 homo sapien
15	426.5	69.5	597	2	Q9BU10_HUMAN	Q9bu10 homo sapien
16	426.5	69.5	597	2	O6GMX5_HUMAN	O6gmx5 homo sapien
17	426.5	69.5	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien
18	422.5	68.8	597	2	Q9BOB8_HUMAN	Q9bqb8 homo sapien
19	417.5	68.0	478	2	Q6NYH3_HUMAN	O6nyh3 homo sapien
20	417	67.9	146	1	HV2I_HUMAN	P06331 homo sapien
21	413	67.3	473	2	Q8TC63_HUMAN	O8tc63 homo sapien
22	386	62.9	116	2	Q7Z3Y6_HUMAN	Q7z3y6 homo sapien
23	383.5	62.5	476	2	O6GMX7_HUMAN	O6gmz7 homo sapien
24	383	62.4	483	2	Q5U413_MOUSE	Q5u413 mus musculus
25	382.5	62.3	479	2	Q9NM22_MOUSE	Q9nm22 mus musculus
26	381.5	62.1	117	1	HV2G_HUMAN	P01825 homo sapien
27	377	61.4	136	2	G6LBO5_MOUSE	O6lbo5 mus musculus
28	375.5	61.2	615	2	Q569B6_RAT	Q569b6 rattus norv
29	371.5	60.5	477	2	Q5I0J1_RAT	Q5i0j1 rattus norv
30	365.5	59.5	119	2	Q53VR3_MOUSE	Q53vr3 mus musculus
31	365	59.4	122	2	Q9UL75_HUMAN	Q9ul75 homo sapien

RESULT 1				
Q6GMX1_HUMAN				
ID	Q6GMX1_HUMAN	PRELIMINARY;	PRT;	476 AA.
AC	Q6GMX1;			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Spleen;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
Proc.	Nat'l. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Spleen;			
RA	Strausberg R.;			
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
EMBL	BC073773; AAH73773.1; -, mRNA.			
GO	GO:0016021; C:integral to membrane; IEA.			
DR	InterPro; IPR003599; IG-like.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG.cl.			
DR	InterPro; IPR003006; IG.MHC.			
DR	InterPro; IPR003596; IG.v.			
DR	Pfam; PF07654; C1-set; 3.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGC1; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 4.			

P01822 mus musculus
Q53vq1 mus musculus
Q652i1 mus musculus
Q569b8 rattus norv
Q53vq5 mus musculus
Q561m5 mus musculus
Q569b3 rattus norv
Q569b3 rattus norv
P01819 mus musculus
Q53vr7 mus musculus
P01823 mus musculus
Q5i0l9 rattus norv
Q9ul96 homo sapien
Q5m839 rattus norv
Q58e54 mus musculus

```
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match      80.2%; Score 492.5; DB 2; Length 476;
Best Local Similarity 74.2%; Pred. No. 1.9e-41;
Matches 92; Conservative 13; Mismatches 6; Indels 13; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVQPPGKLEWIGNIYHSGNTYNP 61
Db 25 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVQPPGKLEWIGNIYHSGNTYNP 84
QY 62 KSRITWSDTSKNHFSRLTSTVTAADTAVYFCARS-----DGYTLDNWGQTLV 110
Db 85 KSRVTSIDTSKNQFSLKXNSVTAADTAVYFCARAGWGSFRSWALDGFNI--WGQ 142
QY 111 TVSS 114
Db 143 TVSS 146

RESULT 2
Q6GMX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAR73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.

Query Match      77.7%; Score 477; DB 2; Length 465;
Best Local Similarity 81.4%; Pred. No. 6.8e-40;
Matches 92; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVQPPGKLEWIGNIYHSGNTYNP 61
Db 25 ESGPGLVKPSQTLSTCTVSGGSI--SGYWSWIRQPPGKLEWIGRIYSGSTYNPSL 82
QY 62 KSRITWSDTSKNHFSRLTSTVTAADTAVYFCARS-----DGYTLDNWGQTLV 114
Db 83 KSRVTSIDTSKNQFSLKSLSVTAADTAVYFCARGRTFYDYGQGTLTVSS 135

RESULT 3
Q72374 HUMAN
ID Q72374 HUMAN PRELIMINARY; PRT; 492 AA.
AC Q72374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538077; CAD98001.1; -, mRNA.
DR HSSP; P01820; 1G7J.
DR SNR; Q72374; 262-470.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760FOCA74B CRC64;

Query Match      77.6%; Score 476.5; DB 2; Length 492;
Best Local Similarity 76.9%; Pred. No. 8.2e-40;
Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVQPPGKLEWIGNIYHSGNTYNP 61
Db 37 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWVQPPGKLEWIGNIYHSGNTYNP 96
QY 62 KSRITWSDTSKNHFSRLTSTVTAADTAVYFCAR----SDGYTLDNWGQTLV 114
Db 97 KSRITVSDTSKNHFSRLTSTVTAADTAVYFCVRHVEGPGW-FDPWGQTLV 152

RESULT 4
Q72379 HUMAN
ID Q72379 HUMAN PRELIMINARY; PRT; 478 AA.
AC Q72379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
```

DR EMBL; AF103795; AAC79084.1; -; mRNA.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; IG7J.
DR SMR; O95973; 20-147.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 VH4 heavy chain variable region.
FT NON TER 150 150
FT SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 150;
Best Local Similarity 76.1%; Pred. No. 2.6e-39;
Matches 86; Conservative 12; Mismatches 15; Indels 0; Gaps 0

QY 2 ESDPGLVKPSQTLSTLCVTSGGIRSQGYKWSVVRQPPGKGLEWIGNIYHSGNTYYNPSL 61
DB 25 ESDPGLVKPSETLSLCTVSGGSISSNTYWGVIQRPPEKGLEWIGLSHNSGSDYNPSP 84
QY 62 KSRITMSVDTSKNHFSLRLTSTVAADTAVYCARSDGYTLDNMQGQTLVTSS 114
DB 85 KSRVTISVDTSKNQFSLRLSSVTAADTAVYCARLGMGAEDFMGHGTMTVTSS 137

RESULT 6
Q96KX8 HUMAN
ID Q56KX8 HUMAN PRELIMINARY; PRT; 496 AA.
AC Q96KX8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
[1]
NP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung.
RX MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalhus D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung.
RP Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC016369; AAH16369.1; -; mRNA.
DR HSSP; P01876; 10W0.
DR SMR; Q96KX8; 266-474.

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DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 496 AA; 53392 MW; D3469229894040D69 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 496;
Best Local Similarity 74.2%; Pred. No. 9.7e-39;
Matches 89; Conservative 10; Mismatches 13; Indels 8; Gaps 2;

QY 2 ESGPGLVKPSQTLTCTVSGGIRSGYWSVRPPGKGLEWIGNIYHSGNTYNPSSL 61
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 ESGPGLVKPSQTLTCTVSGGIRSGYWSVRPPGKGLEWIGNIYHSGNTYNPSSL 84
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRITWSVDSKHFSLRLTSTVTAADTAVYFCARSDGYT-----LDNWGQGLTVTVSS 114
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 KSRVTISVDSKQSLKRLTSTVTAADTAVYFCAR-HGYSRSGRTGAIDYWGQGLTVTVSS 143

RESULT 7
Q9UL73 HUMAN
ID Q9UL73_HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berns S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiootype.";
RL J. Exp. Med. 174:1639-1652(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2511001;
RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
RT "The smaller human VH gene families display remarkably little
RT polymorphism.";
RL EMBO J. 8:3741-3748(1989).
DR ENBL; AF035041; AAD56277.1; -; mRNA.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR SMART; Q9UL73; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR NON_TER 1 1
FT NON_TER 119 119
```

```
SQ SEQUENCE 119 AA; 13219 MW; 1BD886B6420EA0BE CRC64;

Query Match 75.5%; Score 463.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 3.6e-39;
Matches 90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

QY 2 ESGPGLVKPSQTLTCTVSGGIRSGYWSVRPPGKGLEWIGNIYHSGNTYNPSSL 61
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPSQTLTCTVSGGIRSGYWSVRPPGKGLEWIGNIYHSGNTYNPSSL 63
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRITWSVDSKHFSLRLTSTVTAADTAVYFCARSDG---YLDNWGQGLTVTVSS 114
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 KSRVTISVDSKQSLKRLTSTVTAADTAVYFCARLSNMGPFYFDYWGQGLTVTVSS 119

RESULT 8
Q6GMX7 HUMAN
ID Q6GMX7_HUMAN PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073765; AAH3765.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;
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Query Match          74.4%; Score 457; DB 2; Length 477;
Best Local Similarity 77.4%; Pred. No. 7, 6e-38;
Matches 89; Conservative 7; Mismatches 15; Indels 4; Gaps 2;

QY 2 ESGPGLVKPQSLTSLCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGTYNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQTAGKLEWIGVISHSGTNYNPSL 82
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG--YTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 KSRVTLSDTSKNQFSLRLTSVTAADTAVVYCARSSWDFAFDYGQGLTVTVSS 137
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q96EY0 HUMAN
ID Q96EY0 HUMAN PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1904154;
RA Neale G.A., Kitchingman G.R.;
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT chain enhancer region contain a non-translatable exon and are
RT extremely heterogeneous at the 5' end.";
RL Nucleic Acids Res. 19:2427-2433 (1991).
DR EMBL; BC011857; AAH11857.2; -; mRNA.
DR PIR; S15590; S15590.
DR HSSP; P01820; IG70.
DR SMR; Q96EY0; 27-251.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.

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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E9FF27B CRC64;

Query Match          74.4%; Score 457; DB 2; Length 620;
Best Local Similarity 78.0%; Pred. No. 1e-37;
Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;

QY 2 ESGPGLVKPQSLTSLCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGTYNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 32 ESGPGLVKPSETLSLCTVSGGSISS--YVWSWIRQTAGKLEWIGVISHSGTNYNPSL 89
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDN-----WGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 KSRVTVMSVDTSKNQFSLRLTSVTAADTAVVYCA-SQFWELPTVGLFYWGQGLTVTVSS 146
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q6P418 HUMAN
ID Q6P418 HUMAN PRELIMINARY; PRT; 576 AA.
AC Q6P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -; mRNA.
DR HSSP; P01820; 1A7N.
DR Ensembl; ENSG00000196122; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.

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DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; IgG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63364 MW; FB97C949D720F1E CRC64;

Query Match 73.5%; Score 451; DB 2; Length 576;
Best Local Similarity 76.7%; Pred. No. 3.8e-37;
Matches 89; Conservative 7; Mismatches 16; Indels 4; Gaps 2;

QY 2 ESGPGLVKPQTSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTYNNPSL 61
DB 32 ESGPGLVKPQTSLTCAVSGGSISSN-WMSWVWVQPPGKGLWIGNIYHSGNTYNNPSL 90
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSDG---YTLDNWGQGLTVTVSS 114
DB 91 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARSLGDIYYGHVDVWGQGLTVTVSS 146

RESULT 11
HV2F HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=8222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).
CC -1- MISCELLANEOUS: This chain was isolated from an IgD myeloma
protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02099; D2HWA.
DR HSP; P01820; 1G7J.
DR GlycoSuiteDB; P01824; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin v region.
FT DOMAIN 1 113 Ig-like.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.7%; Score 440.5; DB 1; Length 129;
Best Local Similarity 65.1%; Pred. No. 8.6e-37;
Matches 82; Conservative 14; Mismatches 15; Indels 15; Gaps 2;

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QY 2 ESGPGLVKPQTSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSETSLTCTIVSGGPIRTGYWGWIRQPPGKGLWIGVYVYTGSIYNNPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCAR-----SDGYTLDNWGQGT 108
DB 66 RGRVTISVDTSRQFSLNLSMSAADTAVYCARGNPPPYDITGSDDDG--IDVWGQGT 123
QY 109 LVTVSS 114
DB 124 TVTVSS 129

RESULT 12
Q81ZD7_HUMAN
ID Q81ZD7_HUMAN PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AV145445; AAN64329.1; -; mRNA.
DR HSP; P01820; 1G7J.
DR SNR; Q81ZD7; 1-130.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON TER 1 130
FT NON TER 130 130
FT SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 69.9%; Score 429; DB 2; Length 130;
Best Local Similarity 68.8%; Pred. No. 1.3e-35;
Matches 86; Conservative 12; Mismatches 15; Indels 12; Gaps 4;

QY 2 ESGPGLVKPQTSLTCTVSGGSIIRSGGYWVWVQPPGKGLWIGNIYHSGNTY 56
DB 6 QSGPGLVKPSETSLTCTVSGGSISSSYWGWIRQPPGKGLWIGSLYSGTSGSPY 65
QY 57 YNPSLKSRIITMSVDTSKNHFSLRLTSVTAADTAVYCAR---SDG--YT-LDNWGQGT 109
DB 66 YAPSLRSRVIISVDTSKNQLSLRLSSVTAADTAVYCARSPHSCSGGCGYAFFOHWGQGL 125
QY 110 TVTVSS 114
DB 126 TVTVSS 130

RESULT 13
Q86SX2_HUMAN
ID Q86SX2_HUMAN PRELIMINARY; PRT; 139 AA.
AC Q86SX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

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RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=B cells;
RA  Li W.B., Gruber C., Jesse J., Polayes D.;
RL  Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[2]
RN  NUCLEOTIDE SEQUENCE.
RP  TISSUE=B cells;
RA  Genoscope; (FEB-2003) to the EMBL/GenBank/DBJ databases.
RL  Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BX248300; CAD62627.1; -; mRNA.
DR  HSSP; P01820; 1G7J.
DR  SMR; Q868X2; 33-129.
DR  Ensembl; ENSG00000130076; Homo sapiens.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON TER
SQ  SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 69.5%; Score 427; DB 2; Length 139;
Best Local Similarity 85.1%; Pred. No. 2.2e-35;
Matches 80; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY  2  ESGPLVKPQTLTCTVSGGSRGGYYSWVRQPGKLEWIGNIYHSGNTYNPSSL 61
DB  38  ESGPLVKPSETLSLTCTVSGGSISS--YYSWIRQPPGKLEWIGYIYSGSYNPSSL 95

QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR 95
DB  96  KSRVTSVDTSKNQFSLKLSVTAADTAVYYCAR 129

QY  14
O8WUX4_HUMAN
ID  O8WUX4_HUMAN PRELIMINARY; PRT; 595 AA.
AC  O8WUX4;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Hypothetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
[1]
RP  NUCLEOTIDE SEQUENCE.
RC  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,
RA  Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RL  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN  (2)
NUCLEOTIDE SEQUENCE.
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RC  TISSUE=Lymph;
RA  Strausberg R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=89235232; PubMed=2497188;
RA  Sanz I., Casali P., Thomas J.W., Nottkins A.L., Capra J.D.;
RA  "Nucleotide sequences of eight human natural autoantibody VH regions
RT  reveals apparent restricted use of VH families."
J. Immunol. 142:4054-4061 (1989).
DR  EMBL; BC019235; AAH19235.2; -; mRNA.
DR  FIR; G34964; G34964.
DR  HSSP; P01861; IADQ.
DR  SMR; Q8WUX4; 27-256.
DR  Ensembl; ENSG00000130076; Homo sapiens.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF07654; C1-set; 4.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGc1; 4.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PSS0835; IG_LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 595 AA; 65291 MW; 0D4B50776545714E CRC64;

Query Match 69.5%; Score 426.5; DB 2; Length 595;
Best Local Similarity 70.0%; Pred. No. 1.2e-34;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

QY  4  GPGLVKPSQTLTCTVSGGSRGGYYSWVRQPGKLEWIGNIYHSGNTYNPSSLK 63
DB  34  GAGLKPSETLSLTCTVGGSGF--SGYYSWIRQPPGKLEWIGNIHSGNTYNPSSLK 91

QY  64  RITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDG-YTLDNQGQGLTVTVSS 114
DB  92  RVTISVDTSKKQLSKLSVNAADTAVYYCARVITRASPGTDGRYGMVDMVGQGLTVTVSS 151

RESULT 15
O9BU10_HUMAN
ID  O9BU10_HUMAN PRELIMINARY; PRT; 597 AA.
AC  O9BU10;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  IGHM protein.
DE  Name=IGHM;
GN  Homo sapiens (Human).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
[1]
RP  NUCLEOTIDE SEQUENCE.
RC  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lymph;
RC NIH MGC Project;
RG Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL ENBL; BC002963; AA02963.1; -; mRNA.
DR HSP; P01861; IADQ.
DR SMR; Q9BU10; 20-249.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain
KW SEQUENCE 597 AA; 65275 MW; 2DAFA8FB7E055851 CRC64;
Query Match 69.5%; Score 426.5; DB 2; Length 597;
Best Local Similarity 70.0%; Pred. No. 1.2e-34;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;
QY 4 GPGILVPSQTLSTLTCTVSGGSIKSGYNSWVQPPGKGLWIGNIYHSGNTYYPNLSKS 63
DB 27 GAGLLKPESETLSLTCTGVYGGSP--SGYNSWIRQPPGKGLWIGNIHSGSTNYNPNSKS 84
QY 64 RITMSVDTSKNHFSLRLTSVTAADTAVYICAR-----SDG-YTLDNWGQGLTVTVSS 114
DB 85 RVTISVDTSKKQLSLKLSLVNADTAVYICARVITRASPGTDGRYGMVWGGQGLTVTVSS 144

Search completed: April 3, 2006, 14:36:27
Job time : 96.3818 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:36:55 ; Search time 24.3545 Seconds
(without alignments)
386.993 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LBSGPGLVKPSQSLTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/PCBUS COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507	82.6	473	2	US-09-049-672A-4
2	504.5	82.2	117	2	US-10-330-613A-13
3	494	80.5	122	1	US-08-360-125-11
4	494	80.5	122	1	US-08-450-578-11
5	494	80.5	122	1	US-09-017-628-11
6	494	80.5	122	2	US-09-014-880-11
7	494	80.5	122	2	US-08-450-363-11
8	494	80.5	122	2	US-09-467-903-11
9	494	80.5	172	2	US-09-472-087-7
10	494	80.5	172	2	US-09-472-087-86
11	493.5	80.4	117	2	US-10-330-613A-5
12	490.5	79.9	117	2	US-09-720-493-2
13	488.5	79.6	119	2	US-09-025-769B-39
14	488.5	79.6	119	2	US-09-025-769B-65
15	488.5	79.6	119	2	US-09-490-070A-39
16	488.5	79.6	119	2	US-09-490-070A-65
17	488.5	79.6	119	2	US-09-490-153-39
18	488.5	79.6	119	2	US-09-490-153-65
19	488.5	79.6	119	2	US-09-490-324-39
20	488.5	79.6	119	2	US-09-490-324-65
21	488	79.5	118	2	US-09-025-769B-25
22	488	79.5	118	2	US-09-490-070A-25
23	488	79.5	118	2	US-09-490-153-25
24	488	79.5	118	2	US-09-490-324-25
25	487.5	79.4	119	2	US-10-330-613A-25
26	482.5	78.6	121	2	US-10-330-613A-37
27	480.5	78.3	117	2	US-10-330-613A-33

28	478	77.9	487	2	US-09-800-729-145
29	477	77.7	120	1	US-09-424-840B-20
30	473.5	77.1	119	1	US-08-360-125-5
31	473.5	77.1	119	1	US-08-450-578-5
32	473.5	77.1	119	1	US-09-017-628-5
33	473.5	77.1	119	1	US-09-014-880-5
34	473.5	77.1	119	2	US-08-450-363-5
35	473.5	77.1	119	2	US-09-467-903-5
36	468.5	76.3	121	2	US-10-330-613A-9
37	467.5	76.1	121	2	US-10-330-613A-1
38	467.5	76.1	121	1	US-10-330-613A-17
39	459.5	74.8	142	1	US-08-480-774A-2
40	458	74.6	244	2	US-08-918-148-79
41	458	74.6	244	2	US-09-138-091A-77
42	455	74.1	99	2	US-10-194-975-38
43	454.5	74.0	125	2	US-10-432-006-1
44	454	73.9	250	2	US-10-194-975-110
45	453	73.8	99	2	US-10-194-975-36

ALIGNMENTS

RESULT 1
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANCTUT01

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; CLONE: 1513264
US-09-049-672A-4

Query Match      82.6%; Score 507; DB 2; Length 473;
Best Local Similarity 79.8%; Pred. No. 1e-42;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWVWVROPKGLWIGNIYHSGNTYNNPSL 61
Db 25 ESGPGLVKPSETLSLTCVSGGSTRSGGYWVWVROPKGLWIGNIYHSGNTYNNPSL 84
Qy 62 KSRITMSVDTSKNHPSLRLSVTAADTAVYVCARSD-----GYTLDNWQGTLLVTSS 114
Db 85 KSRVTSISVDTSKNQFSLKLSVTAADTAVYVCARDVGLRGNGYMDVWGQGLTLVTSS 143

RESULT 2
US-10-330-613A-13
; Sequence 13, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330.613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match      82.2%; Score 504.5; DB 2; Length 117;
Best Local Similarity 84.2%; Pred. No. 3.4e-43;
Matches 96; Conservative 9; Mismatches 6; Indels 3; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWVWVROPKGLWIGNIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWVWVROPKGLWIGNIYHSGNTYNNPSL 65
Qy 62 KSRITMSVDTSKNHPSLRLSVTAADTAVYVCARSDGYTLDNWQGTLLVTSS 114
Db 66 KSRVTSISVDTSKNQFSLKLSVTAADTAVYVCAREGDDF--DYWGQGTLLVTSS 117

RESULT 3
US-08-360-125-11
; Sequence 11, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-360-125-11

Query Match      80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSTRSGGYWVWVROPKGLWIGNIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSETLSLTCVSGGSTRSGGYWVWVROPKGLWIGNIYHSGNTYNNPSL 65
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;/ TITLE: 80.5%; Score 494; DB 2; Length 122;
;/ JOURNAL: 78.6%; Pred. No. 4.1e-42;
;/ VOLUME: 78.6%; Pred. No. 4.1e-42;
;/ ISSUE: 78.6%; Pred. No. 4.1e-42;
;/ PAGES: 78.6%; Pred. No. 4.1e-42;
;/ DATE: 78.6%; Pred. No. 4.1e-42;
;/ DOCUMENT NUMBER: 78.6%; Pred. No. 4.1e-42;
;/ FILING DATE: 78.6%; Pred. No. 4.1e-42;
;/ PUBLICATION DATE: 78.6%; Pred. No. 4.1e-42;
;/ RELEVANT RESIDUES IN SEQ ID NO: 78.6%; Pred. No. 4.1e-42;
US-08-450-363-11
Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;
Qy 2 ESGPGLVKPSQTLTCTVSGGSISSSSYYGWIQPPGKGLWIGNIYHSGTYNPSL 61
Db 6 ESGPGLVKPSQTLTCTVSGGSISSSSYYGWIQPPGKGLWIGNIYHSGTYNPSL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSD---GYTLDNWGQGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVYCARSGYGGYYGHDVWGQGLTVTVSS 122
RESULT 8
US-09-467-903-11
; Sequence 11, Application US/09467903
; Patent No. 6787153
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; Yoko HIRAKAWA
; No. 6787153hihiko ITO
; Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; Specifically Binding to Surface Antigen of Cancer
; Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/467,903
; FILING DATE: 21-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,363
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER: JP158859/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158860/1991
; FILING DATE: June 28, 1991
; APPLICATION NUMBER: JP158861/1991
; FILING DATE: June 28, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: <Unknown>
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-467-903-11
Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;
Qy 2 ESGPGLVKPSQTLTCTVSGGSISSSSYYGWIQPPGKGLWIGNIYHSGTYNPSL 61
Db 6 ESGPGLVKPSQTLTCTVSGGSISSSSYYGWIQPPGKGLWIGNIYHSGTYNPSL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCARSD---GYTLDNWGQGLTVTVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAADTAVYCARSGYGGYYGHDVWGQGLTVTVSS 122
RESULT 9
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-39

Query Match 79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.4e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
Qy 2 ESGPGLVKPSQTLSTCTVSGSGIRSGYVSWRPPGKLEWIGNIYHSGNTYNPSL 61
Db 6 ESGPGLVKPSETLSLTCTVSGSGISS--YYWSWIRQPPGKLEWIGIYYISGNTYNP 63
Qy 62 KSRITMSVDTSKNHFSLTSTVTAADTAVVYCAR--SDG-YTLDNWGGTGLTVTSS 114
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARWGGDGFYAMDYWGQGLTVTSS 119

RESULT 14
US-09-025-769B-65
Sequence 65, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65
Query Match 79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.4e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
Qy 2 ESGPGLVKPSQTLSTCTVSGSGIRSGYVSWRPPGKLEWIGNIYHSGNTYNP 61
Db 6 ESGPGLVKPSETLSLTCTVSGSGISS--YYWSWIRQPPGKLEWIGIYYISGNTYNP 63
Qy 62 KSRITMSVDTSKNHFSLTSTVTAADTAVVYCAR--SDG-YTLDNWGGTGLTVTSS 114
Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARWGGDGFYAMDYWGQGLTVTSS 119

RESULT 15
US-09-490-070A-39
Sequence 39, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.

```

;
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39

Query Match          79.6%; Score 488.5; DB 2; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.4e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Qy  2  ESGPGLVKPSQTLSLTCTVSGGSTRGGYYWVSWVROPKGLWIGNIYHSGNTYINPSL 61
Db  6  ESGPGLVKPSQTLSLTCTVSGGSISS--YYWSWIRQPPGKGLWIGIYYSGSTINPSL 63

Qy  62  KSRITMSVDTSKNHFSRLTSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTVSS 114
Db  64  KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARWGGDGFYANDYWGQGLTVTVSS 119

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Search completed: April 3, 2006, 14:40:33
Job time : 25.3545 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: April 3, 2006, 15:10:27 ; Search time 77.9 Seconds
(without alignments)
611.458 Million cell updates/sec
Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQGLTVTVSS 114
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	4	US-10-027-725A-8
2	600	97.7	114	4	US-10-027-725A-9
3	546	88.9	114	4	US-10-027-725A-7
4	514.5	83.8	140	5	US-10-893-576-41
5	511	83.2	128	5	US-10-727-155-2
6	511	83.2	128	5	US-10-727-155-10
7	511	83.2	128	5	US-10-727-155-30
8	510.5	83.1	121	4	US-10-309-762-152
9	510	83.1	118	4	US-10-309-762-138
10	509.5	83.0	123	4	US-10-309-762-10
11	507.5	82.7	125	4	US-10-309-762-11
12	507	82.6	120	4	US-10-309-762-13
13	507	82.6	120	4	US-10-309-762-144
14	507	82.6	122	4	US-10-309-762-147
15	506.5	82.5	119	5	US-10-893-576-189
16	506	82.4	221	3	US-09-972-656-80
17	505.5	82.3	121	4	US-10-309-762-151
18	505	82.2	128	5	US-10-727-155-26
19	504.5	82.2	117	4	US-10-330-613-13
20	504.5	82.2	117	4	US-10-330-530-13
21	504.5	82.2	117	4	US-10-660-357-13
22	504	82.1	121	5	US-10-805-177-56
23	503.5	82.0	119	4	US-10-309-762-140
24	503.5	82.0	148	6	US-11-131-648-13
25	503.5	82.0	148	6	US-11-131-648-35
26	503	81.9	125	5	US-10-805-177-53
27	502.5	81.8	123	4	US-10-309-762-12

28	502.5	81.8	144	5	US-10-893-576-35	Sequence 35, Appl
29	502	81.8	122	5	US-10-984-960A-56	Sequence 56, Appl
30	502	81.8	124	4	US-10-309-762-75	Sequence 75, Appl
31	502	81.8	143	4	US-10-309-762-96	Sequence 96, Appl
32	501	81.6	130	6	US-11-009-731-46	Sequence 46, Appl
33	501	81.6	252	3	US-09-880-748-1329	Sequence 1329, Ap
34	501	81.6	252	4	US-10-293-418-1329	Sequence 1329, Ap
35	500	81.4	120	4	US-10-309-762-128	Sequence 128, App
36	500	81.4	120	4	US-10-309-762-137	Sequence 137, App
37	500	81.4	121	4	US-10-308-817-137	Sequence 137, App
38	500	81.4	121	4	US-10-453-698-137	Sequence 6, Appli
39	500	81.4	126	3	US-09-974-449-6	Sequence 18, Appl
40	500	81.4	126	5	US-10-652-502A-18	Sequence 34, Appl
41	499.5	81.4	135	4	US-10-388-214A-34	Sequence 127, App
42	499	81.3	116	4	US-10-309-762-127	Sequence 40, Appl
43	499	81.3	120	5	US-10-706-689-40	Sequence 40, Appl
44	499	81.3	120	5	US-10-988-360-40	Sequence 8, Appli
45	498.5	81.2	125	4	US-10-309-762-8	

ALIGNMENTS

RESULT 1
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-8

Query Match	100.0%;	Score 614;	DB 4;	Length 114;
Best Local Similarity	100.0%;	Pred. No. 8.3e-48;		
Matches 114;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	LESQGLVKPSQTLSTCTVSGSIRSGGYVSWVRQPGKLEWIGNIVHSGNTYNPS	60	
Db	1	LESQGLVKPSQTLSTCTVSGSIRSGGYVSWVRQPGKLEWIGNIVHSGNTYNPS	60	
Qy	61	LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS	114	
Db	61	LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTVSS	114	

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match      97.7%; Score 600; DB 4; Length 114;
Best Local Similarity 96.5%; Pred. No. 1.5e-46;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LESGGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRITMSVDTSKNHFSLRLSSVTAADTAVVYCARSDGYTLDNWGQGLTVTSS 114

RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match      88.9%; Score 546; DB 4; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.1e-41;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LESGGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 LESGGLVKPAQTLSTLSCAVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRITMSVDTSENKFSRLNSVTAADTAVVYCARLDGYTLDIWGQGLTVTSS 114

RESULT 4
US-10-893-576-41
; Sequence 41, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 41
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 2.40.1
; OTHER INFORMATION: Heavy chain V region (Vh, VG 4-31)-huIgG2 C region
```

```
US-10-893-576-41

Query Match      83.8%; Score 514.5; DB 5; Length 140;
Best Local Similarity 84.5%; Pred. No. 9.9e-39;
Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVTSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 KSRITMSVDTSKNQFSLKLSVTAADTAVVYCARSDGYTLDNWGQGLTVTSS 140

RESULT 5
US-10-727-155-2
; Sequence 2, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspai S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-2

Query Match      83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 1.9e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSVRQPPGKGLEWIGNIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDGYTLDNWGQGLTVT 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRITMSVDTSKNQFSLKLSVTAADTAVVYCARSDNQYNWDEVDYGLDVGQGLTVT 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 112 VSS 114
    |||
Db 126 VSS 128

RESULT 6
US-10-727-155-10
; Sequence 10, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
```

```
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-10

Query Match      83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 1.9e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY  2  ESGPGLVKPSQTLSTCTVSGGSIRSGGYWYVWVRQPPGKGLEWIGNIYHSGNTYINPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   6  ESGPGLVKPSQTLSTCTVSGGSIRSGGYWYVWVRQPPGKGLEWIGNIYHSGNTYINPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTLDNWGGQGLTVT 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSDNQYNWDEVDYGLDVGQGLTVT 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  112  VSS 114
    |||||
Db   126  VSS 128
    |||||

RESULT 7
US-10-727-155-30
; Sequence 30, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
```

```
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-30

Query Match      83.2%; Score 511; DB 5; Length 128;
Best Local Similarity 78.9%; Pred. No. 1.9e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

QY  2  ESGPGLVKPSQTLSTCTVSGGSIRSGGYWYVWVRQPPGKGLEWIGNIYHSGNTYINPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   6  ESGPGLVKPSQTLSTCTVSGGSIRSGGYWYVWVRQPPGKGLEWIGNIYHSGNTYINPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG-----YTLDNWGGQGLTVT 111
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSDNQYNWDEVDYGLDVGQGLTVT 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  112  VSS 114
    |||||
Db   126  VSS 128
    |||||

RESULT 8
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match      83.1%; Score 510.5; DB 4; Length 121;
Best Local Similarity 82.8%; Pred. No. 2e-38;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;

QY  2  ESGPGLVKPSQTLSTCTVSGGSIRSGGYWYVWVRQPPGKGLEWIGNIYHSGNTYINPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   6  ESGPGLVKPSQTLSTCTVSGGSIRSGGYWYVWVRQPPGKGLEWIGNIYHSGNTYINPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSD---GYTLDNWGGQGLTVTSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   66  KSRVTISVDTSKNQFSLKLSVTAADTAVVYCAYYDILTGYAFDVGQGLTVTSS 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

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; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match      83.1%; Score 510; DB 4; Length 118;
Best Local Similarity 85.0%; Pred. No. 2.1e-38;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARS-----DGYTLDNWGQGLTLVTSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARYGSGDYWGQGLTLVTSS 118

RESULT 10
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10

Query Match      83.0%; Score 509.5; DB 4; Length 123;
Best Local Similarity 82.2%; Pred. No. 2.5e-38;
Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARS-----DGYTLDNWGQGLTLVTSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARYGSGDYWGQGLTLVTSS 123

RESULT 11
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11

Query Match      82.7%; Score 507.5; DB 4; Length 125;
Best Local Similarity 81.7%; Pred. No. 3.8e-38;
Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARS-----DGYTLDNWGQGLTLVTSS 114
Db 66 KSRITISVDTSKNQFSLKLSVTAADTAVYVCARTYDFLTGYPDADFIMWGQGLTMVTSS 125

RESULT 12
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match      82.6%; Score 507; DB 4; Length 120;
Best Local Similarity 83.6%; Pred. No. 4e-38;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLSTLTCTVSGGSIIRSGGYWWSVRPPGKGLWIGNIYHSGNTYINPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARS---LDNWGQGLTLVTSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCAR-DGYNYWYFDLWGRGLTLVTSS 120

RESULT 13
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
```



```
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match      82.6%; Score 507; DB 4; Length 120;
Best Local Similarity 83.6%; Pred. No. 4e-38;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVQRPPGKLEWIGNIYHSGNTYYNP 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVQRPPGKLEWIGNIYHSGNTYYNP 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT---LDNWGGGLTV 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCAR-DGNYWYFDLWGRGLTV 120

RESULT 14
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

Query Match      82.6%; Score 507; DB 4; Length 122;
Best Local Similarity 82.1%; Pred. No. 4.1e-38;
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVQRPPGKLEWIGNIYHSGNTYYNP 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVQRPPGKLEWIGNIYHSGNTYYNP 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR---SDGYLDNWGGGLTV 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARYDILTGYGMDWGGGLTV 122
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US-10-893-576-189
; Sequence 189, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
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; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 189
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic gamma heavy
; OTHER INFORMATION: chain protein sequence
US-10-893-576-189

Query Match      82.5%; Score 506.5; DB 5; Length 119;
Best Local Similarity 84.2%; Pred. No. 4.4e-38;
Matches 96; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVQRPPGKLEWIGNIYHSGNTYYNP 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIRSGGYWVQRPPGKLEWIGNIYHSGNTYYNP 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT---LDNWGGGLTV 112
Db 66 KSRVTMSVDTSKNQPSLKLSSVTAADTAVYYCARDPLYGDYGFDPWGQGLTV 119

Search completed: April 3, 2006, 15:20:23
Job time : 77.9 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 15:13:12 ; Search time 10.3636 Seconds
(without alignments)
334.861 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LBSPGLVKPQSQTLSLCTV.....RSDGYTLDNWGQTLVTVS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US12 NEW PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US13 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	81.6	252	7 US-11-054-515-1329	Sequence 1329, Ap
2	501	81.6	252	7 US-11-266-444-1329	Sequence 1329, Ap
3	494	80.5	172	7 US-11-128-900-7	Sequence 7, Appl
4	494	80.5	172	7 US-11-128-900-86	Sequence 86, Appl
5	493	80.3	252	7 US-11-054-515-1994	Sequence 1994, Ap
6	493	80.3	252	7 US-11-266-444-1994	Sequence 1994, Ap
7	492.5	80.2	251	7 US-11-054-515-990	Sequence 990, App
8	492.5	80.2	251	7 US-11-266-444-990	Sequence 990, App
9	492.5	80.2	253	7 US-11-054-515-1619	Sequence 1619, Ap
10	492.5	80.2	253	7 US-11-266-444-1619	Sequence 1619, Ap
11	488.5	79.6	119	6 US-10-834-397-39	Sequence 39, Appl
12	488.5	79.6	119	6 US-10-834-397-65	Sequence 65, Appl
13	488	79.5	118	6 US-10-834-397-25	Sequence 25, Appl
14	487	79.3	254	7 US-11-054-515-1578	Sequence 1578, Ap
15	487	79.3	254	7 US-11-266-444-1578	Sequence 1578, Ap
16	487	79.3	256	7 US-11-054-515-1607	Sequence 1607, Ap
17	487	79.3	256	7 US-11-266-444-1607	Sequence 1607, Ap
18	482	78.5	146	6 US-10-721-763-17	Sequence 17, Appl
19	482	78.5	154	6 US-10-721-763-25	Sequence 25, Appl
20	480	78.2	250	7 US-11-054-515-1548	Sequence 1548, Ap
21	480	78.2	250	7 US-11-266-444-1548	Sequence 1548, Ap
22	478	77.9	256	7 US-11-054-515-1745	Sequence 1745, Ap
23	478	77.9	256	7 US-11-266-444-1745	Sequence 1745, Ap
24	477.5	77.8	117	7 US-11-012-353-162	Sequence 162, App
25	475	77.4	116	7 US-11-102-424-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-11-054-515-1329
; Sequence 1329, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 03/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1329
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1329

Query Match 81.6%; Score 501; DB 7; Length 252;

Best Local Similarity 78.5%; Pred. No. 3.9e-36;

Matches 95; Conservative 10; Mismatches 8; Indels 8; Gaps 2;

Qy 2 BSGPLVKPQSQTLSLCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYVPSL 61

Db 6 BSGPLVKPQSQTLSLCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYVPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD-----GYTL----DNWGQTLVTVS 113

Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGDYDILTGYPLHAFDIWKGTLVTVS 125

QY 114 S 114

Db 126 S 126

RESULT 2

US-11-266-444-1329
; Sequence 1329, Application US/11266444
; Publication No. US2005062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: EP523P1d1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1329

Query Match 81.6%; Score 501; DB 7; Length 252;
Best Local Similarity 78.5%; Pred. No. 3.9e-36;
Matches 95; Conservative 10; Mismatches 8; Indels 8; Gaps 2;

QY 2 ESGPLVKPQSLTSLCTVSGGIRSGYWSVRQPPGKLEWIGNIYHSGNTYNP 61

Db 6 ESGPLVKPSETLSLCTVSGGIRSGYWSVRQPPGKLEWIGNIYHSGNTYNP 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSD----GYTL---DNWGGTLVTVS 113

Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGDYDILTGYPLHAFDIWKGTLVTVS 125

QY 114 S 114

Db 126 S 126

RESULT 3

US-11-128-900-7
; Sequence 7, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497

; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-7

Query Match 80.5%; Score 494; DB 7; Length 172;

Best Local Similarity 81.6%; Pred. No. 1.1e-35;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 3 SGFGLVKPQSLTSLCTVSGGIRSGYWSVRQPPGKLEWIGNIYHSGNTYNP 62

Db 1 SGFGLVKPQSLTSLCTVSGGIRSGYWSVRQPPGKLEWIGNIYHSGNTYNP 60

QY 63 SRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG--YTLDNWGGTLVTVS 114

Db 61 SRVTISVDTSKNQFSLKLSVTAADTAVVYCARSDGYDIDWGGTTLVTVS 114

RESULT 4

US-11-128-900-86
; Sequence 86, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-86

Query Match 80.5%; Score 494; DB 7; Length 172;

Best Local Similarity 81.6%; Pred. No. 1.1e-35;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 3 SGFGLVKPQSLTSLCTVSGGIRSGYWSVRQPPGKLEWIGNIYHSGNTYNP 62

Db 1 SGFGLVKPQSLTSLCTVSGGIRSGYWSVRQPPGKLEWIGNIYHSGNTYNP 60

QY 63 SRITMSVDTSKNHFSLRLTSVTAADTAVVYCARSDG--YTLDNWGGTLVTVS 114

Db 61 SRVTISVDTSKNQFSLKLSVTAADTAVVYCARSDGYDIDWGGTTLVTVS 114

RESULT 5

US-11-054-515-1994

; Sequence 1994, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1994

Query Match 80.3%; Score 493; DB 7; Length 252;
Best Local Similarity 78.2%; Pred. No. 1.9e-35;
Matches 93; Conservative 9; Mismatches 11; Indels 6; Gaps 1;

QY 2 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGNTYYPNPSL 61
Db 6 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGNTYYPNPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVSMVDTSKNQYSLKLSVTAADTAVYYCARLRPDADYGDYGFYWGQGTMTVTYSS 124

RESULT 6
US-11-266-444-1994
; Sequence 1994, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1994
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1994

Query Match 80.3%; Score 493; DB 7; Length 252;
Best Local Similarity 78.2%; Pred. No. 1.9e-35;
Matches 93; Conservative 9; Mismatches 11; Indels 6; Gaps 1;

QY 2 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGNTYYPNPSL 61
Db 6 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGNTYYPNPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVSMVDTSKNQYSLKLSVTAADTAVYYCARLRPDADYGDYGFYWGQGTMTVTYSS 124

RESULT 7
US-11-054-515-990
; Sequence 990, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 990
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-990

Query Match 80.2%; Score 492.5; DB 7; Length 251;
Best Local Similarity 76.7%; Pred. No. 2.1e-35;
Matches 92; Conservative 12; Mismatches 9; Indels 7; Gaps 1;

QY 2 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGNTYYPNPSL 61
Db 6 ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVWVQPPGKLEWIGNIYHSGNTYYPNPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVTSVDTSKNQFSLKLSVTAADTAVYYCARFRYDILTYYGYGMDVWGRGTMTVTYSS 125

RESULT 8
US-11-266-444-990
; Sequence 990, Application US/11266444

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; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulatc
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 990
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-990

Query Match      80.2%; Score 492.5; DB 7; Length 251;
Best Local Similarity 76.7%; Pred. No. 2.1e-35;
Matches 92; Conservative 12; Mismatches 9; Indels 7; Gaps 1;

QY  2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVROPKPGKLEWIGNIYHSGNTYINPSL 61
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Db  6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVROPKPGKLEWIGNIYHSGNTYINPSL 65
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----DGYT--LDNWQGGTLVTV 114
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  66  KSRVTISDTSKNQFSLKLSVTAADTAVYYCARFYDILTSYYGMDVWGRGTWTVSS 125
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-11-054-515-1619
; Sequence 1619, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1619
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; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1619

Query Match      80.2%; Score 492.5; DB 7; Length 253;
Best Local Similarity 77.9%; Pred. No. 2.1e-35;
Matches 95; Conservative 9; Mismatches 9; Indels 9; Gaps 2;

QY  2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVROPKPGKLEWIGNIYHSGNTYINPSL 61
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Db  6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVROPKPGKLEWIGNIYHSGNTYINPSL 65
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----DGYT--LDNWQGGTLVTV 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  66  KSRVTISDTSKNQFSLKLSVTAADTAVYYCVRSYYDILTGPRPYTDAPDINGKGLTVV 125
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QY  113  SS 114
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Db  126  SS 127

RESULT 10
US-11-266-444-1619
; Sequence 1619, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1619
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1619

Query Match      80.2%; Score 492.5; DB 7; Length 253;
Best Local Similarity 77.9%; Pred. No. 2.1e-35;
Matches 95; Conservative 9; Mismatches 9; Indels 9; Gaps 2;

QY  2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVROPKPGKLEWIGNIYHSGNTYINPSL 61
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Db  6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWVROPKPGKLEWIGNIYHSGNTYINPSL 65
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QY  62  KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCAR-----DGYT--LDNWQGGTLVTV 112
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Db  66  KSRVTISDTSKNQFSLKLSVTAADTAVYYCVRSYYDILTGPRPYTDAPDINGKGLTVV 125
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QY  113  SS 114
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Db  126  SS 127

RESULT 11
US-10-834-397-39
; Sequence 39, Application US/10834397
; Publication No. US2006000334A1
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;
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;             Pack, Peter
;             Ilag, Vic
;             Ge, Liming
;             Moroney, Simon
;             Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
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; US-10-834-397-39
;
; Query Match 79.6%; Score 488.5; DB 6; Length 119;
; Best Local Similarity 81.9%; Pred. No. 2.3e-35;
; Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
;
; Qy 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPPGKGLEWIGNIYHSGNTYNP 61
; Db 6 ESGPGLVKPSETLSLTCTVSGSIRSGYWSWVRQPPGKGLEWIGNIYHSGNTYNP 63
;
; Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCAR--SDG-YTLDNWGGTLVTYSS 114
; Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYCARWGGDGFYAMDYWGQGLT 119
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; RESULT 12
; US-10-834-397-65
; Sequence 65, Application US/10834397
; Publication No. US20060003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;             Pack, Peter
;             Ilag, Vic
;             Ge, Liming
;             Moroney, Simon
;             Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries

```

```

;
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
;
; US-10-834-397-65
;
; Query Match 79.6%; Score 488.5; DB 6; Length 119;
; Best Local Similarity 81.9%; Pred. No. 2.3e-35;
; Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
;
; Qy 2 ESGPGLVKPSQTLSTCTVSGSIRSGYWSWVRQPPGKGLEWIGNIYHSGNTYNP 61
; Db 6 ESGPGLVKPSETLSLTCTVSGSIRSGYWSWVRQPPGKGLEWIGNIYHSGNTYNP 63
;
; Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYCAR--SDG-YTLDNWGGTLVTYSS 114
; Db 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVYCARWGGDGFYAMDYWGQGLT 119
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; RESULT 13
; US-10-834-397-25
; Sequence 25, Application US/10834397
; Publication No. US20060003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;             Pack, Peter
;             Ilag, Vic
;             Ge, Liming
;             Moroney, Simon
;             Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
;
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/834,397
FILING DATE: 29-Apr-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-834-397-25

Query Match 79.5%; Score 488; DB 6; Length 118;
Best Local Similarity 81.7%; Pred. No. 2.5e-35;
Matches 94; Conservative 7; Mismatches 10; Indels 4; Gaps 2;
QY 2 ESGPGLVKPSETLSLTCTVSGGSI--YVWSIRQPPGKLEWIGNIYHSGNTYNP 61
DB 6 ESGPGLVKPSETLSLTCTVSGGSI--YVWSIRQPPGKLEWIGNIYHSGNTYNP 63
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSGDY-----TLDNWGGT 114
DB 64 KSRVTISMDTSKNQFSLNLSVTAADTAVYVCARGKGYDILTGYRDNWFDPWGRG 118

RESULT 14
US-11-054-515-1578
Sequence 1578, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1578
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1578

Query Match 79.3%; Score 487; DB 7; Length 254;
Best Local Similarity 75.0%; Pred. No. 6.2e-35;
Matches 93; Conservative 9; Mismatches 10; Indels 12; Gaps 2;
QY 2 ESGPGLVKPSETLSLTCTVSGGSI--SSGYWGWVPPGKLEWIGNIYHSGNTYNP 61
DB 6 ESGPGLVKPSETLSLTCTVSGGSI--SSGYWGWVPPGKLEWIGNIYHSGNTYNP 64
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSGDY-----TLDNWGGT 110
DB 65 KSRVTISMDTSKNQFSLNLSVTAADTAVYVCARGKGYDILTGYRDNWFDPWGRG 124
QY 111 TVSS 114
DB 125 TVSS 128

RESULT 15
US-11-266-444-1578
Sequence 1578, Application US/11266444
Publication No. US2006062789A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523P1D1
CURRENT APPLICATION NUMBER: US/11/266,444
CURRENT FILING DATE: 2005-11-04
PRIOR APPLICATION NUMBER: 09/880,746
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1578
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-266-444-1578

Query Match 79.3%; Score 487; DB 7; Length 254;
Best Local Similarity 75.0%; Pred. No. 6.2e-35;
Matches 93; Conservative 9; Mismatches 10; Indels 12; Gaps 2;
QY 2 ESGPGLVKPSETLSLTCTVSGGSI--SSGYWGWVPPGKLEWIGNIYHSGNTYNP 61
DB 6 ESGPGLVKPSETLSLTCTVSGGSI--SSGYWGWVPPGKLEWIGNIYHSGNTYNP 64
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSGDY-----TLDNWGGT 110
DB 65 KSRVTISMDTSKNQFSLNLSVTAADTAVYVCARGKGYDILTGYRDNWFDPWGRG 124
QY 111 TVSS 114
DB 125 TVSS 128

us-10-027-725a-8.rapbn

Mon Apr 3 16:31:44 2006

Search completed: April 3, 2006, 15:21:29
Job time : 10.3636 secs

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:09 ; Search time 99.1455 Seconds
(without alignments)
505.209 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQTLVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605	98.5	114	5	ABG30447 Human IGE
2	600	97.7	114	5	ABG30446 Human IGE
3	556	90.6	114	5	ABG30445 Human IGE
4	524.5	85.4	121	7	ADP03982 Murine-ex
5	524	85.3	118	7	ADP03968 Murine-ex
6	523.5	85.3	123	7	ADP03870 Murine-ex
7	521	84.9	120	7	ADP03874 Murine-ex
8	521	84.9	120	7	ADP03873 Murine-ex
9	521	84.9	122	7	ADP03977 Murine-ex
10	521	84.9	473	4	AAB36206 Human imm
11	520	84.7	221	7	ADJ32126 Human int
12	519.5	84.6	121	7	ADP03981 Murine-ex
13	519.5	84.6	125	7	ADP03871 Murine-ex
14	517.5	84.3	119	7	ADP03970 Murine-ex
15	516.5	84.1	123	2	AAW78433 Antibody
16	516.5	84.1	123	5	ABB97976 Heavy cha
17	516.5	84.1	123	7	ADG88414 anti-Ob-R
18	516.5	84.1	123	7	ADP03872 Murine-ex
19	516.5	84.1	144	9	ADX98263 Human ant
20	516	84.0	124	7	ADP03935 Murine-ex
21	515.5	84.0	117	7	ADC99784 Anti-huma
22	515.5	84.0	117	7	ADQ05388 Anti-MUC1
23	515.5	84.0	117	7	ADF09826 Human ant
24	515	83.9	125	8	ADS16556 Human ant

25	514	83.7	120	7	ADP03958 Murine-ex
26	514	83.7	120	7	ADP03969 Murine-ex
27	514	83.7	121	7	ADJ80377 Antibody
28	514	83.7	121	8	ADS16559 Human ant
29	514	83.7	122	9	AEA21492 Human ant
30	513.5	83.6	120	4	AAB62775 Murine-ex
31	513	83.6	116	7	ADP03957 Murine-ex
32	512.5	83.5	125	7	ADP03868 Murine-ex
33	512.5	83.5	125	7	ADP03876 Murine-ex
34	512.5	83.5	480	9	ADZ57697 Anti-cMet
35	512	83.4	123	4	AAB62745 Human HIV
36	511.5	83.3	119	7	ADP03961 Murine-ex
37	511.5	83.3	140	9	ADX98269 Human ant
38	511	83.2	110	7	ADP03934 Murine-ex
39	510.5	83.1	122	4	AAB62765 Murine-ex
40	510.5	83.1	123	7	ADP03869 Murine-ex
41	510.5	83.1	127	7	ADP03874 Murine-ex
42	510.5	83.1	148	9	ADX98259 Human ant
43	510	83.1	246	3	RAY15126 Anti-muri
44	509	82.9	149	9	ADZ57713 Germ-line
45	508.5	82.8	123	9	ADX98417 Human ant

ALIGNMENTS

RESULT 1
ABG30447
ID ABG30447 standard; protein; 114 AA.
XX
AC ABG30447;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IGE Fab clone 100 heavy chain protein.
XX
KW Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KW Timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX (PRAA) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX N-PSDB; ABK89639.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising

PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.

XX
PS Disclosure; Page 38; 45pp; English.

CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergenic patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC fab, clone 100 heavy chain protein of the invention

XX
SQ Sequence 114 AA;

Query Match 98.5%; Score 605; DB 5; Length 114;
Best Local Similarity 99.1%; Pred. No. 3.9e-44;
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTCTGSGSIRSGGYYSWIRQPPGKGLEWIGYIYHSGNTYNP 60
DB 1 LESGPGLVKPSQTLSTCTCTGSGSIRSGGYYSWIRQPPGKGLEWIGYIYHSGNTYNP 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQTLTVSS 114
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQTLTVSS 114

RESULT 2
ABG30446
ID ABG30446 standard; protein; 114 AA.
AC ABG30446;
XX
XX 21-OCT-2002 (first entry)
XX Human IgE Fab clone 60 heavy chain protein.
XX Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
XX timothy grass pollen allergen; passive immunotherapy.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95
FT /note= "FR3 region"
FT Region 96. .103
FT /note= "CDR2 region"
FT Region 104. .114
FT /note= "FR4 region"

XX W0200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.
PR (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI: 2002-583604/62.
DR N-PSDB; ABR89638.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.

XX
PS Disclosure; Page 37; 45pp; English.

CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergenic patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC fab, clone 60 heavy chain protein of the invention

XX
SQ Sequence 114 AA;

Query Match 97.7%; Score 600; DB 5; Length 114;
Best Local Similarity 96.5%; Pred. No. 1e-43;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTCTGSGSIRSGGYYSWIRQPPGKGLEWIGYIYHSGNTYNP 60
DB 1 LESGPGLVKPSQTLSTCTCTGSGSIRSGGYYSWIRQPPGKGLEWIGYIYHSGNTYNP 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQTLTVSS 114
DB 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQTLTVSS 114

RESULT 3
ABG30445
ID ABG30445 standard; protein; 114 AA.
XX
XX ABG30445;
XX
XX 21-OCT-2002 (first entry)
XX Human IgE Fab clone 94 heavy chain protein.
XX Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
XX timothy grass pollen allergen; passive immunotherapy.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Region 1. .26
FT /note= "FR1 region"
FT Region 27. .33
FT /note= "CDR1 region"
FT Region 34. .47
FT /note= "FR2 region"
FT Region 48. .63
FT /note= "CDR2 protein"
FT Region 64. .95

PT Region /note= "FR3 region"
FT 96..103
PT /note= "CDR2 region"
FT 104..114
PT /note= "FR4 region"
FT
PN WO200253595-A1.
XX
XX 11-JUL-2002.
PD
XX 27-DEC-2001; 2001WO-S0002908.
PF
XX 29-DEC-2000; 2000SE-00004892.
PR
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
PA
XX Flicker S, Steinberger P, Kraft D, Valenta R;
PI
XX WPI; 2002-583604/62.
DR
XX N-PSDB; ABK89637.
DX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 36; 45pp; English.
PS
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to phi p 2. The present sequence represents the human IgG
CC fab, clone 94 heavy chain protein of the invention
XX
SQ Sequence 114 AA;
Query Match 90.6%; Score 556; DB 5; Length 114;
Best Local Similarity 90.4%; Pred. No. 6e-40;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 1 LESGPGLVKPSQTLTLCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 60
Db 1 LESGPGLVKPAQTLSLCAVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 60
Qy 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD---GYTLDMGQGLTVTVSS 114
Db 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARLDGTLTLDIMGQGLTVTVSS 114
RESULT 4
ADP03982
ID ADP03982 standard; protein; 121 AA.
XX
XX ADP03982;
AC
XX 29-JUL-2004 (first entry)
DT
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
DE
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytostatic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; breast cancer;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;

gene therapy; murine; mouse; human; heavy chain variable domain.
KW Unidentified.
OS
XX WO2003048328-A2.
PN
XX 12-JUN-2003.
PD
XX 02-DEC-2002; 2002WO-US038550.
PF
XX 03-DEC-2001; 2001US-0337275P.
PR
XX (ABGE-) ABGENIX INC.
PA
XX Gudas J, Foltz I, Handa M, Gallo M;
PI WPI; 2003-523295/49.
DR
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
PT
PS Example 2; SEQ ID NO 152; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 121 AA;
Query Match 85.4%; Score 524.5; DB 7; Length 121;
Best Local Similarity 86.2%; Pred. No. 3.2e-37;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
Qy 2 ESGPGLVKPSQTLTLCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIIRSGGYWWSWIRQHPGKLEWIGYIYHSGNTYNP 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD---GYTLDMGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTAADTAVVYCARSD---GYTLDMGQGLTVTVSS 121
RESULT 5
ADP03968
ID ADP03968 standard; protein; 118 AA.
XX
XX ADP03968;
AC
XX 29-JUL-2004 (first entry)
DT
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
DE
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytostatic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX Unidentified.
OS
XX WO2003048328-A2.
PN
XX

PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Example 2; SEQ ID NO 138; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 118 AA;
Query Match 85.3%; Score 524; DB 7; Length 118;
Best Local Similarity 88.5%; Pred. No. 3.4e-37;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 2 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPGKLEWIGYIHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPGKLEWIGYIHSGNTYNP 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARS-----DGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARYGSGSDYWGQGLTVTVSS 118
RESULT 6
ADP03870
ID ADP03870 standard; protein; 123 AA.
XX
AC ADP03870;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytostatic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX

PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 10; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 123 AA;
Query Match 85.3%; Score 523.5; DB 7; Length 123;
Best Local Similarity 85.6%; Pred. No. 3.9e-37;
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;
QY 2 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPGKLEWIGYIHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPGKLEWIGYIHSGNTYNP 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARS-----DGYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARYGSGSDYWGQGLTVTVSS 123
RESULT 7
ADP03974
ID ADP03974 standard; protein; 120 AA.
XX
AC ADP03974;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytostatic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 XX Example 2; SEQ ID NO 144; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.

XX Sequence 120 AA;

Query Match 84.9%; Score 521; DB 7; Length 120;
 Best Local Similarity 87.1%; Pred. No. 6.3e-37;
 Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPGKLEWIGYHSGNTYNP 61
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPGKLEWIGYHSGNTYNP 65
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT---LDNMGGQGLTVTVSS 114
 DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-DGYNYWYFDLMGRGLTVTVSS 120

RESULT 8

ADP03873
 ID ADP03873 standard; protein; 120 AA.

XX AC ADP03873;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX WO2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 XX Claim 1; SEQ ID NO 13; 89pp; English.

CC The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.

XX Sequence 120 AA;

Query Match 84.9%; Score 521; DB 7; Length 120;
 Best Local Similarity 87.1%; Pred. No. 6.3e-37;
 Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPGKLEWIGYHSGNTYNP 61
 DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWWSWIRQPGKLEWIGYHSGNTYNP 65
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT---LDNMGGQGLTVTVSS 114
 DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-DGYNYWYFDLMGRGLTVTVSS 120

RESULT 9

ADP03977
 ID ADP03977 standard; protein; 122 AA.

XX AC ADP03977;

XX DT 29-JUL-2004 (first entry)

XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
 XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.

XX OS Unidentified.

XX WO2003048328-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038550.

XX PR 03-DEC-2001; 2001US-0337275P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J, Foltz I, Handa M, Gallo M;

XX DR WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 147; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating a tumour,

CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 122 AA;

Query Match 84.9%; Score 521; DB 7; Length 122;
Best Local Similarity 85.5%; Pred. No. 6.4e-37;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYNP 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCAR----SDGYTLDNWQGTTLTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARYDYDILTGYGMDVWGQGTTLTVSS 122

RESULT 10
AAB36206
ID AAB36206 standard; protein; 473 AA.
AC AAB36206;
XX
XX 15-FEB-2001 (first entry)
XX Human immune system associated protein HISAP-4.
XX Human; immune system associated protein; HISAP-4; immune disorder;
KW infection; autoimmune disease; cancer.
XX Homo sapiens.
XX US6135941-A.
XX 24-OCT-2000.
XX 27-MAR-1998; 98US-00049672.
XX 27-MAR-1998; 98US-00049672.
XX (INCY-) INCYTE PHARM INC.
XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX WPI; 2001-030926/04.
DR N-PSDB; AAC66522.
XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
XX Claim 1; Col 53-56; 54pp; English.

CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 473 AA;

Query Match 84.9%; Score 521; DB 4; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.6e-36;

Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYNP 61
DB 25 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYNP 84
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCAR----SDGYTLDNWQGTTLTVSS 114
DB 85 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARDVGLRGNGYGMVWGQGTTLTVSS 143

RESULT 11
ADJ32126
ID ADJ32126 standard; protein; 221 AA.
AC ADJ32126;
XX
XX 22-APR-2004 (first entry)
XX Human interferon-gamma antibody heavy chain amino acid sequence SeqID80.
XX antibody; antigen binding domain; interferon-gamma; INF-gamma;
KW antagonist antibody; antiinflammatory; immunosuppressive;
KW autoimmune disease; inflammatory condition; human; heavy chain.
XX Homo sapiens.
XX US2003099647-A1.
XX 29-MAY-2003.
XX 05-OCT-2001; 2001US-00972656.
XX 05-OCT-2001; 2001US-00972656.
XX (DESH/) DESHPANDE R V.
PA (TSAI/) TSAI M.
XX Deshpande RV, Tsai M;
XX WPI; 2003-696068/66.
DR N-PSDB; ADJ32125.
XX New antibody or antigen binding domain, or its fragment, variant or
PT derivative, which binds to an interferon-gamma protein, useful for
PT preparing a composition for preventing or treating inflammatory or
PT autoimmune disorders.
XX Claim 10; SEQ ID NO 80; 113pp; English.

CC This invention relates to a novel antibody or antigen binding domain, or
CC its fragment, variant or derivative, which binds to an interferon-gamma
CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
CC useful for the development of compounds with an antiinflammatory or
CC immunosuppressive activity through action as interferon-gamma agonists. A
CC composition containing the antibody is useful for preventing or treating
CC an autoimmune disease and an inflammatory condition. The present sequence
CC is that of an antibody heavy chain of a human IFN-gamma antibody which
CC may be part of the invention.
XX
SQ Sequence 221 AA;

Query Match 84.7%; Score 520; DB 7; Length 221;
Best Local Similarity 86.7%; Pred. No. 1.4e-36;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSGIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYNP 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWQGTTLTVSS 114
DB 66 KSRVTISVDRSKNQFSLKLSVTAADTAVYVCARGDWGYFDYWGQGTTLTVSS 118

AC	A DP03871;
XX	29-JUL-2004 (first entry)
DT	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
DE	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX	cystosatic; colorectal neoplasm; renal cell carcinoma;
KW	cervical intraepithelial squamous neoplasia;
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	Unidentified.
DS	WO2003048328-A2.
XX	12-JUN-2003.
XX	02-DEC-2002; 2002WO-US038550.
PFF	03-DEC-2001; 2001US-033727SP.
PR	(ABGE-) ABGENIX INC.
XX	Gudas J, Foltz I, Handa M, Gallo M;
XPI	WPI; 2003-523295/49.
DR	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PPT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PPT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
PPT	Claim 1; SEQ ID NO 11; 89pp; English.
PS	The invention relates to a novel isolated monoclonal antibody (mAb)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated via the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	Sequence 125 AA;
SQ	Query Match 84.6%; Score 519.5; DB 7; Length 125;
	Best Local Similarity 83.3%; Pred. No. 8.8e-37;
	Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2
QY	2 ESGPGLVKPSQTLSLCTVSSGGIRSGGYWSWIROPKGLEWTGIYHSGNTYYNPSL 61
DB	: : : : : : : : : :
	6 ESGPGLVKPSQTLSLCTVSSGGISGGYWSWIROHPGKGLEWTGIYYSNGTYNPSL 65
	: : : : : : : : :
QY	62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARS-----DGV--TLDNWGGTTLVTYSS 114
	: : : : : : : : :
DB	66 KSRITISVDTSKNQFSLKLSSVTAADTAVVICARTYDFLTGPDAFDINGGQTWTYSS 125
	: : : : : : : : :
RESULT 14	
ID	ADP03970
AC	ID ADP03970 standard; protein; 119 AA.
XX	
AC	ADP03970;
DT	29-JUL-2004 (first entry)
XX	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.
DE	
XX	

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytostatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial squamous neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX Unidentified.
 XX WO2003048328-A2.
 PN
 XX
 XX 12-JUN-2003.
 PD
 XX
 XX 02-DEC-2002; 2002WO-US038550.
 PF
 XX
 XX 03-DEC-2001; 2001US-0337275P.
 PR
 XX
 XX (ABGE-) ABGENIX INC.
 PA
 XX
 XX Gudas J, Foltz I, Handa M, Gallo M;
 PI
 XX
 XX WPI; 2003-523295/49.
 DR
 XX
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 CC colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 CC intraepithelial squamous and glandular neoplasia or esophageal tumors.
 PT
 XX
 XX Example 2; SEQ ID NO 140; 89pp; English.
 PS
 XX
 XX The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytostatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 XX
 XX Sequence 119 AA;
 SQ
 Query Match 84.3%; Score 517.5; DB 7; Length 119;
 Best Local Similarity 86.8%; Pred. No. 1.2e-36;
 Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
 QY 2 ESGPGLVKPSQTLSTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIHSGNTYYNPSL 61
 DB 6 ESGPGLVKPSQTLSTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIHSGNTYYNPSL 65
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD--GYTLDMWGQGLTVTVSS 114
 DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGNYYYGMDVWGQGLTVTVSS 119
 RESULT 15
 AA78433
 ID AAW78433 standard; protein; 123 AA.
 AC AAW78433;
 XX
 XX 11-MAY-1999 (first entry)
 DT
 XX
 XX Antibody heavy chain targeted to obr clone 26.
 DE
 XX
 XX Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
 KW diagnosis; cancer; primer; PCR; amplification; dicistronic.
 XX
 XX Synthetic.
 OS
 XX
 XX WO98050431-A2.
 PN

XX 12-NOV-1998.
 PD
 XX 30-APR-1998; 98WO-US008762.
 PF
 XX
 XX 02-MAY-1997; 97US-00850058.
 PR
 XX 24-JUN-1997; 97US-0050661P.
 PA
 XX (GETH) GENENTECH INC.
 XX
 XX Arathoon R, Carter PJ, Merchant AM, Presta LG;
 PI
 XX
 XX WPI; 1999-070091/06.
 DR
 XX
 XX Selective preparation of multispecific antibodies - with heteromultimeric
 CC heavy chain and common light chain components, useful for, e.g. in vivo
 CC diagnosis of cancer.
 PT
 XX
 XX Example 4; Fig 5; 69pp; English.
 PS
 XX
 XX This sequence represents the heavy chain variable region for an antibody
 CC that binds to the obr clone 26 protein. The sequence encoding the chain
 CC is generated by a new method for preparing a multispecific Ab comprising
 CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP
 CC comprises a multimerisation domain (MD) forming an interface positioned
 CC to interact with an interface of a MD of the extra PP; and (ii) the first
 CC and extra PPs each have a binding domain, which comprises a heavy chain
 CC and a light chain, where the variable light chains of the first and extra
 CC PPs comprise a common sequence. The method comprises: (a) culturing a
 CC host cell comprising nucleic acid encoding the first PP and extra PP, and
 CC the variable light chain, such that the nucleic acid is expressed; and
 CC (b) recovering the multispecific Ab from the culture. The method prepares
 CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins
 CC and Ab-immunoadhesin chimeras. The method allows for the enhanced
 CC formation of the desired heteromultimer relative to the undesired
 CC heteromultimers and homomultimers. The Abs can be used in immunoassays
 CC and for the in vitro or in vivo diagnosis of various diseases, such as
 CC cancer
 XX
 XX Sequence 123 AA;
 SQ
 Query Match 84.1%; Score 516.5; DB 2; Length 123;
 Best Local Similarity 84.0%; Pred. No. 1.6e-36;
 Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;
 QY 1 LESGPGLVKPSQTLSTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIHSGNTYYNPS 60
 DB 5 VESGPGLVKPSQTLSTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIHSGNTYYNPS 64
 QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD----GYTLDMWGQGLTVTVSS 114
 DB 65 LKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARVDLEDYSGSGADYWGQGLTVTVSS 123
 Search completed: April 3, 2006, 14:27:03
 Job time : 101.145 secs

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:27:40 ; Search time 16.2364 Seconds
(without alignments)
675.565 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501.5	81.7	135	2 S78051	Ig heavy chain pre
2	497.5	81.0	147	2 S13519	Ig heavy chain v r
3	492.5	80.2	140	2 I37782	Ig variable region
4	490	79.8	130	2 S30534	Ig heavy chain v r
5	488.5	79.6	116	2 S37456	Ig mu chain - huma
6	487.5	79.4	130	2 S31690	Ig heavy chain v r
7	480.5	78.3	121	2 S41113	Ig heavy chain v r
8	479.5	78.1	155	2 S31511	Ig heavy chain - h
9	477.5	77.8	146	2 S09710	Ig heavy chain v r
10	477.5	77.8	155	2 S31512	Ig heavy chain - h
11	473.5	77.1	146	2 S09711	Ig heavy chain v r
12	472.5	77.0	127	2 S39668	Ig heavy chain v r
13	472.5	77.0	128	2 S31514	Ig heavy chain - h
14	472	76.9	137	2 S31676	Ig heavy chain v r
15	469	76.4	99	2 S26803	Ig heavy chain v r
16	467.5	76.1	123	2 S30530	Ig heavy chain v r
17	467	76.1	99	2 S26801	Ig heavy chain v r
18	467	76.1	122	2 S69912	Ig V-D-J region (N
19	465	75.7	139	2 S31586	Ig heavy chain v r
20	464	75.6	99	2 S26802	Ig heavy chain v r
21	461	75.1	145	2 S78055	Ig heavy chain pre
22	460.5	75.0	109	2 P11673	Ig heavy chain v r
23	459	74.8	110	2 S44110	Ig heavy chain v-D
24	458	74.6	139	2 A41287	Ig heavy chain pre
25	457	74.4	118	2 A26340	Ig heavy chain pre
26	454	73.9	97	2 P10118	Ig heavy chain V-I
27	454	73.9	99	2 S26899	Ig heavy chain v r
28	452	73.6	135	2 S31604	Ig heavy chain v r
29	451	73.5	118	2 S20780	Ig heavy chain v r

30 451 73.5 129 2 S44114 Ig heavy chain v r
31 448 73.0 99 2 S12418 Ig heavy chain v r
32 447.5 72.9 139 2 S31696 Ig heavy chain v r
33 445.5 72.6 137 2 S31585 Ig heavy chain v r
34 445.5 72.6 140 2 A49045 Ig heavy chain v r
35 445 72.5 120 2 P70370 Ig mu chain precu
36 444 72.3 126 2 S47010 Ig heavy chain V4.
37 443 72.1 99 2 S26800 Ig heavy chain v r
38 442 72.0 99 2 S12412 Ig lambda chain v
39 442 72.0 105 2 S44125 Ig heavy chain v r
40 442 72.0 118 2 S24443 Ig heavy chain pre
41 442 72.0 140 2 S78052 Ig heavy chain v r
42 441.5 71.9 98 2 S12421 Ig heavy chain v r
43 441.5 71.9 132 2 A38911 Ig heavy chain v r
44 441.5 71.9 140 2 A24770 hypothetical hybri
45 441 71.8 97 2 S26906 Ig heavy chain v r

ALIGNMENTS

RESULT 1

S78051
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78051; S23716
R;Harindranath, N

submitted to the EMBL Data Library, August 1990

A;Reference number: S78051

A;Accession: S78051

A;Molecule type: mRNA

A;Residues: 1-135 <HAR>

A;Cross-references: UNIPARC:UPI0000115E87; EMBL:X54437; NID:ig37814; PIDN:CAA38306.1; PID:
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins,
Int. Immunol. 3, 865-875, 1991

A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hi
patient.

A;Reference number: S23716; MUID:92031262; PMID:1718404

A;Accession: S23716

A;Molecule type: mRNA

A;Residues: 13-111 <HAW>

A;Cross-references: UNIPARC:UPI00001769D5; EMBL:X54437

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>

F;14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>

F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 501.5; DB 2; Length 135;

Best Local Similarity 82.2%; Pred. No. 2.8e-38;

Matches 97; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIRSGYVSWIRQPPGKLEWIGYIYHSGNTYFNPSL 61

Db 18 ESGPGLVKPSQTLSTCTVSGGSIRSGYVSWIRQPPGKLEWIGYIYHSGNTYFNPSL 77

Qy 62 KSRVTMSVDTSKHFSLRLSSVTAADTAVVYCAR--SDGYTLDN---WGQGTTLVTVSS 114

Db 78 KSRVTISVDTSKQFSLKLSVTAADTAVVYCARLGPDPDYYLDGMDVWGQGTTLVTVSS 135

RESULT 2

S13519

Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S13519

R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: UNIPARC:UPI0000115EB5; EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;
Best Local Similarity 82.8%; Pred. No. 7e-38;
Matches 96; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 61
DB 32 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 91

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----DGYTLDNWGQGLTVTVSS 114
DB 92 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARPLWFGELFDYWGQGLTVTVSS 147

RESULT 3
I37782
IG variable region (VDJ) (clone T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: I37782; S25476
R;Demailson, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by H
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: UNIPARC:UPI0000176E83; EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 492.5; DB 2; Length 140;
Best Local Similarity 82.2%; Pred. No. 1.9e-37;
Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 61
DB 25 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 82

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----GYTLDNWGQGLTVTVSS 114
DB 83 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARHNSSSWYGRYFDYWGQGLTVTVSS 140

RESULT 4
S30534
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: UNIPARC:UPI0000113F45; EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 490; DB 2; Length 130;
Best Local Similarity 78.4%; Pred. No. 2.9e-37;
Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----YT-----LDNWGQGLT 109
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDXGFWGSGYYTRNSRAAFDIWGQGT 125

QY 110 VTVSS 114
DB 126 VTVSS 130

RESULT 5
S37456
IG mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from I
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MCI>
A;Cross-references: UNIPARC:UPI00001161C0; EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 488.5; DB 2; Length 116;
Best Local Similarity 81.2%; Pred. No. 3.5e-37;
Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

QY 6 GLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 65
DB 1 GLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 60

QY 66 TMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGYT-----LDNWGQGLTVTVSS 114
DB 61 TISVDTSKNQFSLKLSVTAADTAVYYCARG-CYSYGYYYTMDVWGKGTITVTVSS 116

RESULT 6
S31690
IG heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: UNIPARC:UPI0000116471; EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 130;
Best Local Similarity 78.7%; Pred. No. 4.8e-37;
Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 61
DB 11 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNP 68

```

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDG-----YTLDNWGGGTLVTV 112
Db 69 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSSVLLWFGELLYYFDYWGQGLTVTV 128

Qy 113 SS 114
   ||
Db 129 SS 130

RESULT 7
S44113
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44113
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S44113
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <HAW>
A:Cross-references: UNIPARC:UPI000011662F; EMBL:Z31389; NID:9472967; PIDN:CAA83264.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 480.5; DB 2; Length 121;
Best Local Similarity 80.2%; Pred. No. 1.9e-36;
Matches 93; Conservative 6; Mismatches 14; Indels 3; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 6 ESGPGLVKPSETLSLTCTVSGGYSRSSYWGWRQPPGKLEWIGSYSGSYVNP 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCAR-SDGY--TLDNWGGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRVTLSDTSKNQFSLKLSVTAADTGVYCSRLSGGYSDFDYWSQGLTVTVSS 121

RESULT 8
S31511
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31511
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31511
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 479.5; DB 2; Length 155;
Best Local Similarity 77.5%; Pred. No. 3.1e-36;
Matches 93; Conservative 8; Mismatches 10; Indels 9; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGYIYTGSAVNPPL 95

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDG-----YTLDNWGGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 96 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGGGSISSWYDYGMVWGGGTVTVSS 155

RESULT 9
S09710
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A:Reference number: S09710; MUID:90262535; PMID:2111699
A:Accession: S09710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <HUG>
A:Cross-references: UNIPARC:UPI0000115E6C; GB:X52110; NID:931447; PIDN:CAA36344.1; PID:93
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 146;
Best Local Similarity 74.0%; Pred. No. 4.4e-36;
Matches 91; Conservative 11; Mismatches 10; Indels 11; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 25 ESGPGLVKPSETLSLTCTVSGGVSQGLYWGWRQPPGKLEWIGSYFSGSYVNP 84

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDGY-----TLDNWGGGTLTV 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 KSRVTISVDTLKNFSLKLSVTAADTAVVYCTR-PCYGDTSVTKRVNMDLWQGTITV 143

Qy 112 VSS 114
   |||
Db 144 VSS 146

RESULT 10
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31512
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:933082; PIDN:CAA49494.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 155;
Best Local Similarity 76.7%; Pred. No. 4.6e-36;
Matches 92; Conservative 9; Mismatches 10; Indels 9; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGYIYTGSAVNPPI 95

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDG-----YTLDNWGGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 96 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGGGSISSWYVYGMVWGGGTVTVSS 155

RESULT 11
S09711
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
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Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDG-----YTLDNWGGGTLVTV 112
Db 69 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARSSVLLWFGELLYYFDYWGQGLTVTV 128

Qy 113 SS 114
   ||
Db 129 SS 130

RESULT 7
S44113
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44113
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S44113
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <HAW>
A:Cross-references: UNIPARC:UPI000011662F; EMBL:Z31389; NID:9472967; PIDN:CAA83264.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 480.5; DB 2; Length 121;
Best Local Similarity 80.2%; Pred. No. 1.9e-36;
Matches 93; Conservative 6; Mismatches 14; Indels 3; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 6 ESGPGLVKPSETLSLTCTVSGGYSRSSYWGWRQPPGKLEWIGSYSGSYVNP 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCAR-SDGY--TLDNWGGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KSRVTLSDTSKNQFSLKLSVTAADTGVYCSRLSGGYSDFDYWSQGLTVTVSS 121

RESULT 8
S31511
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31511
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31511
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: UNIPARC:UPI00001160FF; EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 479.5; DB 2; Length 155;
Best Local Similarity 77.5%; Pred. No. 3.1e-36;
Matches 93; Conservative 8; Mismatches 10; Indels 9; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGYIYTGSAVNPPL 95

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDG-----YTLDNWGGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 96 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGGGSISSWYDYGMVWGGGTVTVSS 155

RESULT 9
S09710
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A:Reference number: S09710; MUID:90262535; PMID:2111699
A:Accession: S09710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <HUG>
A:Cross-references: UNIPARC:UPI0000115E6C; GB:X52110; NID:931447; PIDN:CAA36344.1; PID:93
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 146;
Best Local Similarity 74.0%; Pred. No. 4.4e-36;
Matches 91; Conservative 11; Mismatches 10; Indels 11; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 25 ESGPGLVKPSETLSLTCTVSGGVSQGLYWGWRQPPGKLEWIGSYFSGSYVNP 84

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDGY-----TLDNWGGGTLTV 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 KSRVTISVDTLKNFSLKLSVTAADTAVVYCTR-PCYGDTSVTKRVNMDLWQGTITV 143

Qy 112 VSS 114
   |||
Db 144 VSS 146

RESULT 10
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31512
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: UNIPARC:UPI00001160F9; EMBL:X69860; NID:933082; PIDN:CAA49494.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 477.5; DB 2; Length 155;
Best Local Similarity 76.7%; Pred. No. 4.6e-36;
Matches 92; Conservative 9; Mismatches 10; Indels 9; Gaps 2;

Qy 2 ESGPGLVKPQSOTLSLTCTVSGGSRGGYYSWIRQPPGKLEWIGYIYHSGNTYVNP 61
Db 38 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKLEWIGYIYTGSAVNPPI 95

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSDG-----YTLDNWGGGTLVTVSS 114
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 96 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARGGGSISSWYVYGMVWGGGTVTVSS 155

RESULT 11
S09711
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
```

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C;Accession: S09711
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-146 <HUG>
A;Cross-references: UNIPARC:UPI0000176CD3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;
Best Local Similarity 73.8%; Pred. No. 1e-35;
Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNPSSL 61
DB 25 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNPSSL 84

QY 62 KSRVTMSVDTSKNHFSRLSLSSVTAADTAVYYCAR-----SDGYTLDNWGQGLTVTV 112
DB 85 RSRVTISVDTSKNQFSLKGLSVTAADTAVYYCARVLVSRTSISQSYMDVWGKGTITV 144

QY 113 SS 114
DB 145 SS 146

RESULT 12
S19668
Ig heavy chain V region (VH4DJH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C;Accession: S19668; S24445
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19668
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: UNIPARC:UPI0000176C7F; EMBL:X61648
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24445
A;Molecule type: mRNA
A;Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F', <JON>
A;Cross-references: UNIPARC:UPI0000115FE7; EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;
Best Local Similarity 74.6%; Pred. No. 1e-35;
Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNPSSL 61
DB 6 QSGSGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGSVHSGFTYNPSSL 65

QY 62 KSRVTMSVDTSKNHFSRLSLSSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTV 112
DB 66 KSRVTMSVDTSKNQFSLKGLSVTAADTAVYYCARSGGTSWRSYKHYMDVWGKGLTVTV 125

QY 113 SS 114
DB 126 SS 127
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RESULT 13
S31514
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: UNIPARC:UPI00001160FB; EMBL:X69862; NID:g33086; PIDN:CAA49496.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;
Best Local Similarity 78.4%; Pred. No. 1e-35;
Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNPSSL 61
DB 13 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIAHIAHIFSGSTYNPFL 72

QY 62 KSRVTMSVDTSKNHFSRLSLSSVTAADTAVYYCAR---SDGYTLDNWGQGLTVTVSS 114
DB 73 KSRVTISVDTSENQFSLRLTSVTPADTAVYYCARIGYNFGYDFDPWGQGLTVTVSS 128

RESULT 14
S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676
R;Quisiner, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CU>
A;Cross-references: UNIPARC:UPI0000116461; EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;
Best Local Similarity 82.8%; Pred. No. 1.3e-35;
Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGYIYHSGNTYNPSSL 61
DB 25 ESGPGLVKPSQTLSTLCTVSGGSIIRSGGYWMIROPPGKLEWIGRIYTSSTYNPSSL 82

QY 62 KSRVTMSVDTSKNHFSRLSLSSVTAADTAVYYCARSDG---YTLDNWGQGLTVTVSS 114
DB 83 KSRVTMSVDTSKNQFSLKGLSVTAADTAVYYCARDAPLMYGMVDVWGQGLTVTVSS 137

RESULT 15
S26803
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26803
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
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A:Reference number: S26800; MUID:92201299; PMID:1348029
A:Accession: S26803
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WEN>
A:Cross-references: UNIPARC:UPI000116485; EMBL:Z14238; NID:937710; PIDN:CAA78607.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match	76.4%	Score	469;	DB	2;	Length	99;
Best Local Similarity	92.6%	Pred. NO.	1.7e-35;				
Matches	87;	Conservative	4;	Mismatches	3;	Indels	0;
						Gaps	0;

QY	2	ESGPGLVKPSQTL	SLTCTVSGSIRSGYVWSWIROP	PGKLEWIGYVHSGNTYINPSL	61
Db	6	ESGPGLVKPSQTL	SLTCTVSGSISGDIYVWSWIROP	PGKLEWIGYVHSGNTYINPSL	65
QY	62	KSRVTMSVDTSKNHFS	LRSLSSVTAADTAVYYCAR	95	
Db	66	KSRVTISVDTSKNQPS	LKLSVTAADTAVYYCAR	99	

Search completed: April 3, 2006, 14:38:06
Job time : 17.2364 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:37 ; Search time 96.3818 Seconds
(without alignments)
834.496 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQTLVTSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504.5	82.2	476	2	Q6GMX1_HUMAN
2	480	78.2	465	2	Q6GMX6_HUMAN
3	480	78.2	478	2	Q7Z379_HUMAN
4	470.5	76.6	119	2	Q9UL73_HUMAN
5	469.5	76.5	492	2	Q7Z374_HUMAN
6	469	76.4	477	2	Q6GMX7_HUMAN
7	468	76.2	150	2	Q95973_HUMAN
8	460	74.9	496	2	Q96KV8_HUMAN
9	460	74.9	620	2	Q96EY0_HUMAN
10	452	73.6	576	2	Q6P418_HUMAN
11	441	71.8	139	2	Q86SX2_HUMAN
12	439.5	71.6	129	1	HV2F_HUMAN
13	431	70.2	130	2	Q81ZD7_HUMAN
14	429.5	70.0	595	2	Q8WU4_HUMAN
15	429.5	70.0	597	2	Q9BU10_HUMAN
16	429.5	70.0	597	2	Q6GMX5_HUMAN
17	429.5	70.0	625	2	Q96AA6_HUMAN
18	425.5	69.3	597	2	Q9BQ88_HUMAN
19	424.5	69.1	478	2	Q6NYH3_HUMAN
20	420	68.4	146	1	HV2I_HUMAN
21	412	67.1	473	2	Q8TC63_HUMAN
22	393.5	64.1	117	1	HV2G_HUMAN
23	393	64.0	483	2	Q5U413_MOUSE
24	392.5	63.9	479	2	Q99M22_MOUSE
25	389	63.4	116	2	Q7Z3Y6_HUMAN
26	387	63.0	136	2	Q6LBO5_MOUSE
27	377.5	61.5	476	2	Q6MZX7_HUMAN
28	377.5	61.5	615	2	Q569B6_RAT
29	375.5	61.2	119	2	Q53VR3_MOUSE
30	372.5	60.7	137	1	HV46_MOUSE
31	370.5	60.3	262	2	Q65Z11_MOUSE

32	369.5	60.2	590	2	Q569B8_RAT	Q569B8_rattus norv
33	368.5	60.0	477	2	Q510J1_RAT	Q510J1_rattus norv
34	367.5	59.9	115	2	Q53VQ1_MOUSE	Q53VQ1_mus musculu
35	365.5	59.5	119	2	Q53VQ5_MOUSE	Q53VQ5_mus musculu
36	364	59.3	122	2	Q9UL75_HUMAN	Q9UL75_homo sapien
37	361	58.8	120	2	Q53VR7_MOUSE	Q53VR7_mus musculu
38	357.5	58.2	113	1	HV47_MOUSE	P01823_mus musculu
39	353.5	57.6	98	2	Q53VR2_MOUSE	Q53VR2_mus musculu
40	353.5	57.6	119	2	Q53VQ9_MOUSE	Q53VQ9_mus musculu
41	352	57.3	485	2	Q561M5_MOUSE	Q561M5_mus musculu
42	349.5	56.9	144	1	HV43_MOUSE	P01819_mus musculu
43	348.5	56.8	116	1	HV61_MOUSE	P18532_mus musculu
44	348	56.7	591	2	Q510I9_RAT	Q510I9_rattus norv
45	347	56.5	117	1	HV62_MOUSE	P18533_mus musculu

ALIGNMENTS

RESULT 1
Q6GMX1_HUMAN
ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.M., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC073773; AAH73773.1; -, mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match      82.2%; Score 504.5; DB 2; Length 476;
Best Local Similarity 76.6%; Pred. No. 2.9e-43;
Matches 95; Conservative 12; Mismatches 4; Indels 13; Gaps 2;

QY 2  ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRPPGKLEWIGYVHSGNTYNP 61
DB 25  ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRPPGKLEWIGYVHSGNTYNP 84
QY 62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDGYTLDNWGQGLTVTVSS 110
DB 85  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARAGVSGFRSWAIDGFNI--WGQGTWV 142
QY 111 TVSS 114
DB 143 TVSS 146

RESULT 2
Q6GNX6 HUMAN
ID Q6GNX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GNX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC073766; AAH73766.1; -; mRNA.
GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
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```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match      78.2%; Score 480; DB 2; Length 465;
Best Local Similarity 84.1%; Pred. No. 9.4e-41;
Matches 95; Conservative 3; Mismatches 13; Indels 2; Gaps 1;

QY 2  ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRPPGKLEWIGYVHSGNTYNP 61
DB 25  ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRPPGKLEWIGYVHSGNTYNP 82
QY 62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDGYTLDNWGQGLTVTVSS 114
DB 83  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARGRFTFDYWGQGLTVTVSS 135

RESULT 3
Q7Z379 HUMAN
ID Q7Z379 HUMAN PRELIMINARY; PRT; 478 AA.
AC Q7Z379;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BX538066; CAD97996.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q7Z379; 248-456.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;

Query Match      78.2%; Score 480; DB 2; Length 478;
Best Local Similarity 77.4%; Pred. No. 9.7e-41;
Matches 89; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

QY 2  ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRPPGKLEWIGYVHSGNTYNP 61
DB 24  ESGPGLVKPSQTLSTCTVSGGSTRSGGYWWSWIRPPGKLEWIGYVHSGNTYNP 83
QY 62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDGY--TLDNWGQGLTVTVSS 114
DB 84  ESRLSISIDTSKNQFSLRLNSLTAAADTAVYFCARGVGLGTFADYWGQGLTVTVSS 138

RESULT 4
Q9UL73 HUMAN
ID Q9UL73 HUMAN PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
```

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1660528;
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosein C., Smith A.,
 RA Diamond B.;
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idiotype";
 RL J. Exp. Med. 174:1639-1652(1991).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2511001;
 RA Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
 RA "The smaller human VH gene families display remarkably little
 RT polymorphism";
 RL EMBL; AF035041; AA56227.1; -; mRNA.
 DR PIR; PH0876; PH0876.
 DR PIR; S12416; S12416.
 DR HSP; P01820; IGTJ.
 DR SMR; Q9UL73; 1-119.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420A0BE CRC64;
 Query Match 76.6%; Score 470.5; DB 2; Length 119;
 Best Local Similarity 79.3%; Pred. No. 2e-40;
 Matches 92; Conservative 8; Mismatches 11; Indels 5; Gaps 2;
 Qy 2 ESGPGLVKPSQTLTCTVSGSIRSGYVSWIRPPGKGLWIGYIYHSGNTYTPSL 61
 Db 6 ESGPGLVKPSQTLTCTVSGSICS--YVSWIRPPGKGLWIGYIYHSGNTYTPSL 63
 Qy 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYVCARS--YTLDNWGQGLTVTVSS 114
 Db 64 KSRVTISVDRSKNHFSLRLSVTAADTAVYCARLSNWGPFYFDWGQGLTVTVSS 119
 RESULT 5
 Q72374 HUMAN
 ID Q72374 HUMAN PRELIMINARY; PRT; 492 AA.
 AC Q72374;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFP686C02218 (Fragment).
 GN Name=DKFP686C02218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BX538077; CAD98001.1; -; mRNA.
 DR HSP; P01820; IGTJ.
 DR SMR; Q72374; 262-470.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 492
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
 Query Match 76.5%; Score 469.5; DB 2; Length 492;
 Best Local Similarity 76.9%; Pred. No. 1.2e-39;
 Matches 90; Conservative 10; Mismatches 12; Indels 5; Gaps 2;
 Qy 2 ESGPGLVKPSQTLTCTVSGSIRSGYVSWIRPPGKGLWIGYIYHSGNTYTPSL 61
 Db 37 ESGPGLVKPSQTLTCTVSGSIRSGYVSWIRPPGKGLWIGYIYHSGNTYTPSL 96
 Qy 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYCAR---SDGYTLDNWGQGLTVTVSS 114
 Db 97 KSRLLTFVDTSKNHFSLRLSVTAADTAVYCVRRHVEGPGYGV-FDPWGQGLTVTVSS 152
 RESULT 6
 Q6GMX7 HUMAN
 ID Q6GMX7 HUMAN PRELIMINARY; PRT; 477 AA.
 AC Q6GMX7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gramwood J., Schmutz J., Myers R.N.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073765; AAH73765.1; -; mRNA.
DR SMR; Q6GKX7; 247-455.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Query Match 76.4%; Score 469; DB 2; Length 477;
Best Local Similarity 80.0%; Pred. No. 1.3e-39;
Matches 92; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGGYWWSWIROPKGLGWIGYIYHSGNTYNP 61
DB 25 ESGPGLVKPSQTLSTCTVSGGIRSGGYWWSWIROPKGLGWIGYIYHSGNTYNP 82
QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYVCARSDG--YTLNMGQGLTLVTSS 114
DB 83 KSRVTLSDTSKNQFSLRLSVTAADTAVYVCARSGSDPFPDYGQGLTLVTSS 137

RESULT 7
O95973 HUMAN
ID O95973 HUMAN PRELIMINARY; PRT; 150 AA.
AC O95973;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VH4 heavy chain variable region precursor (Fragment).
GN Names-IgM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1718404;
RA Harindranath N., Goldfarb I.S., Ikenatsu H., Burastero S.E.,
RA Wilder R.L., Notkins A.L., Casali P.;
RT "Complete sequence of the genes encoding the VH and VL regions of low-
RT and high-affinity monoclonal IgM and IgA1 rheumatoid factors produced
RT by CD5+ B cells from a rheumatoid arthritis patient.";
RL Int. Immunol. 3:865-875(1991).
DR ENBL; AF103795; AAC79084.1; -; mRNA.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSP; P01820; IGJ.
DR SMR; O95973; 20-147.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Signal.
SQ SIGNAL 1 19 Potential.

FT CHAIN 20 >150 VH4 heavy chain variable region.
SQ NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
Query Match 76.2%; Score 468; DB 2; Length 150;
Best Local Similarity 78.8%; Pred. No. 4.6e-40;
Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 2 ESGPGLVKPSQTLSTCTVSGGIRSGGYWWSWIROPKGLGWIGYIYHSGNTYNP 61
DB 25 ESGPGLVKPSQTLSTCTVSGGIRSGGYWWSWIROPKGLGWIGYIYHSGNTYNP 84
QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYVCARSDG--YTLNMGQGLTLVTSS 114
DB 85 KSRVTLSDTSKNQFSLRLSVTAADTAVYVCARSGSDPFPDYGQGLTLVTSS 137

RESULT 8
Q96KX8 HUMAN
ID Q96KX8 HUMAN PRELIMINARY; PRT; 496 AA.
AC Q96KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1718404;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC016369; AAH16369.1; -; mRNA.
DR HSP; P01876; IOWO.
DR SMR; Q96KX8; 266-474.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 496 AA; 53392 MW; D346929849040D69 CRC64;

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-sec; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 58125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 74.9%; Score 460; DB 2; Length 620;
Best Local Similarity 80.5%; Pred. No. 1.5e-38;
Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps

QY 2 ESGPGLVPKPSQTLSLTCTVSGSIRSGGYNSWIRPPKGKLEWTGIYHSGNTYYNPSL 61
DB 32 ESGPGLVPKPSQTLSLTCTVSGSIRSGGYNSWIRPPKGKLEWTGIYHSGNTYYNPSL 61
QY 62 KSRVTMSVDTSKNFSLRLSSVTAADTAVYCARSDGYTLDN-----WGQGFLTVTVSS 114
DB 90 KSRVTMSVDTSKNFSLRLSSVTAADTAVYCA-SQPWELPTVGIFYNGQGLTVTVSS 146

RESULT 10
Q6P418 HUMAN
ID Q6P418 HUMAN PRELIMINARY; PRT; 576 AA.

AC Q6P418; 2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE -
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
XP [1]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marustina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Raha S.S., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailis D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC063384; AAH63384.1; -; mRNA.
DR HSSP; P01820; IA7N.
DR Ensembl; ENSG00000196122; Homo sap.ens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; C1-set; 1.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00407; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.  
SQ SEQUENCE 576 AA; 53364 MW; FB597C949D720F1E CRC64;  
  
Query Match 73.6%; Score 452; DB 2; Length 576;  
Best Local Similarity 77.6%; Pred. No. 9.1e-38;  
Matches 90; Conservative  
2; Gaps 2;  
  
Qy 2 ESGPGLVKPQSTLSLTCTVSGGSIIRSGGYWMIQPPGKLEWIGYIYHSGNTYNP 61  
Db 32 ESGPGLVKPSTLSLTCAVSGGSISSN-WMSWVRQPPGKLEWIGYIYHSGNTYNP 90  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSDG---YTLDNWGQGLTVTVSS 114  
Db 91 KSRVTISVDKSKNQFSLKLSVTAADTAVYICASLDGIYYGHDVWGQGLTVTVSS 146  
  
RESULT 11  
Q86SX2_HUMAN  
ID Q86SX2_HUMAN PRELIMINARY; PRT; 139 AA.  
AC Q86SX2;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Full-length cDNA clone CS0DL004YM19 of B cells (Ramos cell line) of  
DE Homo sapiens (human) (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=B cells;  
RA Li W.B., Gruber C., Jessee J., Polayes D.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=B cells;  
RA Genoscope;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX248300; CAD62627.1; -; mRNA.  
DR HSP; P01820; IG7J.  
DR SNR; Q86SX2; 33-129.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig v.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
FT NON_TER 1  
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;  
  
Query Match 71.8%; Score 441; DB 2; Length 139;  
Best Local Similarity 89.4%; Pred. No. 2.5e-37;  
Matches 84; Conservative 5; Mismatches 3; Indels 2; Gaps 1;  
  
Qy 2 ESGPGLVKPQSTLSLTCTVSGGSIIRSGGYWMIQPPGKLEWIGYIYHSGNTYNP 61  
Db 38 ESGPGLVKPSTLSLTCTVSGGSISSN--YWSWVRQPPGKLEWIGYIYHSGNTYNP 95  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR 95  
Db 96 KSRVTISVDKSKNQFSLKLSVTAADTAVYICAR 129  
  
RESULT 12  
HV2F_HUMAN
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ID HV2F_HUMAN STANDARD; PRT; 129 AA.  
AC P01824;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V-II region WAH.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=8222235; PubMed=6806818;  
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;  
RT *Complete amino acid sequence of the delta heavy chain of human  
RT immunoglobulin D.*;  
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854 (1982).  
CC -I- MISCELLANEOUS: This chain was isolated from an IgD myeloma  
CC protein.  
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC -----  
CC PIR; A02099; D2HUWA.  
DR HSP; P01820; IG7J.  
DR GlycoSuiteDB; P01824; -.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig v.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT DOMAIN 1 113 Ig-like.  
FT NON_TER 129 129  
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;  
  
Query Match 71.6%; Score 439.5; DB 1; Length 129;  
Best Local Similarity 66.7%; Pred. No. 3.3e-37;  
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;  
  
Qy 2 ESGPGLVKPQSTLSLTCTVSGGSIIRSGGYWMIQPPGKLEWIGYIYHSGNTYNP 61  
Db 6 ESGPGLVKPSTLSLTCTVSGGPIRTGYWMIQPPGKLEWIGYIYHSGNTYNP 65  
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICAR-----SDGYTLDNWGQGT 108  
Db 66 RGRVTISVDTSRQFSLRLSRMSAADTAMTYCARGNPPYDICTGSDDG--IDVWGQGT 123  
Qy 109 LVTYSS 114  
Db 124 TVHSS 129  
  
RESULT 13  
Q81ZD7_HUMAN  
ID Q81ZD7_HUMAN PRELIMINARY; PRT; 130 AA.  
AC Q81ZD7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-thyroglobulin heavy chain variable region (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.
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OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Jang Y.-J., Chung J., Park J.-Y.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AV145445; AAN64329.1; -, mRNA.
DR	HSSP; P01820; I67J.
DR	SMR; Q81ZD7; 1-130.
DR	Ensembl; ENSG00000130076; Homo sapiens.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS00835; IG-LIKE; 1.
FT	NON_TER 1
FT	NON_TER 130 130
SQ	SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;
	Query Match 70.2%; Score 431; DB 2; Length 130;
	Best Local Similarity 71.2%; Pred. No. 2.5e-36;
	Matches 89; Conservative 8; Mismatches 16; Indels 12; Gaps 4;
QY	2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYTMSWIRQPFGKLEWIGVIYHSGNT-----Y 56 : : : : : : : : : : :
Db	6 QSGPGLVKPSQTLSLTCTVSGGISSSSYWGIRSQSPGKLEWIGSLYYSGSYSGSPY 65 : : : : : : : : : :
QY	57 YNPFLSKRSVTSDTSKNHFSLRLSSVTAADTAVYYCAR-----SDG--YT-LDNWGGGTLL 109 : : : : : : : : : :
Db	66 YAPFLSRSVIISVDTSKNQLSLRLSSVTAADTAVYYCASPTHCSGGCGYAFFQHGGGGL 125 : : : : : : : : : :
QY	110 VTVSS 114
Db	126 VTVSS 130
RESULT 14	
QBWX4_HUMAN	
ID	QBWX4_HUMAN PRELIMINARY; PRT; 595 AA.
AC	QBWX4;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RP	[1]
RN	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Lymph;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Boasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA	Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;
ET	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC002963; AH02963.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q9BU10; 20-249.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain
SQ SEQUENCE 597 AA; 65275 MW; 2DAFA8FB7E055851 CRC64;

Query Match 70.0%; Score 429.5; DB 2; Length 597;
Best Local Similarity 72.5%; Pred. No. 2e-35;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGLVKPSQTLSTCTVSGSIRSGGYWYQPPKGLGWIGYIHSGNTYINPFLKS 63
DB 27 GAGLLKPSSETLSLTCGYIGGSF--SGYYSWIRQPPKGLGWIGYIHSGNTYINPFLKS 84

QY 64 RVTMSVDTSKNHFSRLSLSSVTAADTAVYCAR-----SDG-YTLDNWQQTIVTVSS 114
DB 85 RVTISVDTSKKQLSLKSSVNAADTAVYCARVITRASPGTDGRYGMWQQTIVTVSS 144

Search completed: April 3, 2006, 14:36:27
Job time : 98.3818 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:36:55 ; Search time 24.3545 Seconds
(without alignments)
386.993 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQTLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	2	US-09-049-672A-4
2	515.5	84.0	117	2	US-10-330-613A-13
3	508	82.7	172	2	US-09-472-087-7
4	508	82.7	172	2	US-09-472-087-86
5	507.5	82.7	117	2	US-10-330-613A-5
6	502.5	81.8	119	2	US-09-025-769B-39
7	502.5	81.8	119	2	US-09-025-769B-65
8	502.5	81.8	119	2	US-09-490-070A-39
9	502.5	81.8	119	2	US-09-490-070A-65
10	502.5	81.8	119	2	US-09-490-153-39
11	502.5	81.8	119	2	US-09-490-153-65
12	502.5	81.8	119	2	US-09-490-324-39
13	502.5	81.8	119	2	US-09-490-324-65
14	497.5	81.0	119	2	US-10-330-613A-25
15	496	80.8	122	1	US-08-360-125-11
16	496	80.8	122	1	US-08-450-578-11
17	496	80.8	122	1	US-09-017-628-11
18	496	80.8	122	1	US-09-014-880-11
19	496	80.8	122	2	US-08-450-363-11
20	496	80.8	122	2	US-09-467-903-11
21	494.5	80.5	121	2	US-10-330-613A-37
22	492.5	80.2	117	2	US-09-720-493-2
23	492.5	80.2	117	2	US-10-330-613A-33
24	492	80.1	487	2	US-09-800-729-145
25	491	80.0	118	2	US-09-025-769B-25
26	491	80.0	118	2	US-09-490-070A-25
27	491	80.0	118	2	US-09-490-153-25

28	491	80.0	118	2	US-09-490-324-25
29	491	80.0	120	2	US-09-424-840B-20
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31	487.5	79.4	119	1	US-08-450-578-5
32	487.5	79.4	119	1	US-09-017-628-5
33	487.5	79.4	119	1	US-09-014-880-5
34	487.5	79.4	119	2	US-08-450-363-5
35	487.5	79.4	119	2	US-09-467-903-5
36	482.5	78.6	121	2	US-10-330-613A-9
37	481.5	78.4	121	2	US-10-330-613A-1
38	481.5	78.4	121	2	US-10-330-613A-17
39	472	76.9	244	2	US-08-918-148-79
40	472	76.9	244	2	US-09-138-091A-77
41	469	76.4	99	2	US-10-194-975-38
42	467	76.1	99	2	US-10-194-975-36
43	467	76.1	99	2	US-10-194-975-39
44	467	76.1	99	2	US-10-330-613A-45
45	467	76.1	99	2	US-10-330-613A-57

ALIGNMENTS

RESULT 1

US-09-049-672A-4

; Sequence 4, Application US/09049672A

; Patent No. 6135941

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yue, Henry

; APPLICANT: Au-Young, Janice

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/049,672A

; FILING DATE: HEREWITH

; CLASSIFICATION: 536

; PRIOR APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0497 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 473 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: PANCTUT01

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CLONE: 1513264
US-09-049-672A-4

Query Match      84.9%; Score 521; DB 2; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.3e-44;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2  ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25  ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----GYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARDVGLRGNGYGMVWGQGLTVTVSS 143

RESULT 2
US-10-330-613A-13
; Sequence 13, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: GUDAS, JEAN
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-13

Query Match      84.0%; Score 515.5; DB 2; Length 117;
Best Local Similarity 86.8%; Pred. No. 1.6e-44;
Matches 99; Conservative 7; Mismatches 5; Indels 3; Gaps 2;

QY 2  ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6  ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR-SDGYTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCAREGDP--DYWGQGLTVTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-5
```

```
US-09-472-087-7

Query Match      82.7%; Score 508; DB 2; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.4e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 3  SGFGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSLK 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1  SGFGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSLK 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63  SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61  SRVTISVDTSKNQFSLKLSVTAADTAVYYCARDSDGYTGIDVWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      82.7%; Score 508; DB 2; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.4e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 3  SGFGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSLK 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1  SGFGLVKPSQTLTCTVSGGSISSGGYYSWIRQPPGKLEWIGYIYHSGNTYNNPSLK 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63  SRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG--YTLDNWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61  SRVTISVDTSKNQFSLKLSVTAADTAVYYCARDSDGYTGIDVWGQGLTVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-10-330-613A-5
; Sequence 5, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: GUDAS, JEAN
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-5
```

```
Query Match      82.7%; Score 507.5; DB 2; Length 117;
Best Local Similarity 86.8%; Pred. No. 1e-43; 7; Indels 3; Gaps 2;
Matches 99; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

QY 2 ESGPGLVKPSQTLTLCTVSGGSIIRGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIIRGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGDGYKY--WGQGLTVTVSS 117

RESULT 6
US-09-025-769B-39
; Sequence 39, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025.769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-39

Query Match      81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLTLCTVSGGSIIRGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIIRGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGDFYAMDYWGQGLTVTVSS 119
```

```
RESULT 7
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025.769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-65

Query Match      81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSQTLTLCTVSGGSIIRGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPGLVKPSQTLTLCTVSGGSIIRGGYWSWIRQPPGKLEWIGYIYHSGNTYINPSL 63

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTVSS 114
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGDFYAMDYWGQGLTVTVSS 119

RESULT 8
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;; White & McAuliffe
;; STREET: 1666 K Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20006
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/490,070A
;; FILING DATE: 24-Jan-2000
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Colin G. Sandercock, Esq.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37629-0005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 912-2000
;; TELEFAX: (202) 912-2020
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 5; Gaps 3;

QY 2 ESGPGLVKPSQTLTCTVSGGSIRSGGYWWSWIRQPPGKGLWIGYIYHSGNTYNPSSL 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLWIGYIYSGSTNPSSL 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCAR--SDG-YTLDNWGQGLTVTVSS 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARWGCGDFYAMDYWGQGLTVTVSS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-09-490-070A-65
; Sequence 65, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/490,070A
;; FILING DATE: 24-Jan-2000
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Colin G. Sandercock, Esq.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37629-0005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 912-2000
;; TELEFAX: (202) 912-2020
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65

Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 5; Gaps 3;

QY 2 ESGPGLVKPSQTLTCTVSGGSIRSGGYWWSWIRQPPGKGLWIGYIYHSGNTYNPSSL 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGPGLVKPSETLSLTCTVSGGSISS--YYWSWIRQPPGKGLWIGYIYSGSTNPSSL 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCAR--SDG-YTLDNWGQGLTVTVSS 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KSRVTISVDTSKNQFSLKLSVTAADTAVVYCARWGCGDFYAMDYWGQGLTVTVSS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-09-490-153-39
; Sequence 39, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794

```
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-153-39
Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSTLSLTCTVSGGSIRSGGYWMSWIRQPPGKGLWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSTLSLTCTVSGGSISS--YYMSWIRQPPGKGLWIGYIYSGSTNPN 63

QY 62 KSRVTMSVDTSKNHFSRLSSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTV 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARWGSGDGFYAMDYWGQGLTVTV 119

RESULT 11
US-09-490-153-65
; Sequence 65, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-FEB-1998
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65
Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSTLSLTCTVSGGSIRSGGYWMSWIRQPPGKGLWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSTLSLTCTVSGGSISS--YYMSWIRQPPGKGLWIGYIYSGSTNPN 63

QY 62 KSRVTMSVDTSKNHFSRLSSVTAADTAVYYCAR--SDG-YTLDNWGQGLTVTV 114
DB 64 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARWGSGDGFYAMDYWGQGLTVTV 119

RESULT 12
US-09-490-324-39
; Sequence 39, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39
Query Match 81.8%; Score 502.5; DB 2; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.3e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 ESGPGLVKPSTLSLTCTVSGGSIRSGGYWMSWIRQPPGKGLWIGYIYHSGNTYNP 61
DB 6 ESGPGLVKPSTLSLTCTVSGGSISS--YYMSWIRQPPGKGLWIGYIYSGSTNPN 63
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LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match 80.8%; Score 496; DB 1; Length 122;
Best Local Similarity 81.2%; Pred. NO. 1.5e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;
Qy 2 ESGPLVKPSTLSLTCTVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSGNTYINPSL 61
Db 6 ESGPLVKPSTLSLTCTVSGSIRSGGYWMSWIRQPGKLEWIGYIYHSGNTYINPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYTCARSD----GYTLDNWCGGTLVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTAADTAVYTCARSGSGYGYGMDVWCGGTLVTVSS 122

Search completed: April 3, 2006, 14:40:32
Job time : 24.3545 secs

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OM protein - protein search, using sw model

Run on: April 3, 2006, 15:10:27 ; Search time 77.9 Seconds
(without alignments)
611.458 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 40 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	4	US-10-027-725A-9
2	600	97.7	114	4	US-10-027-725A-8
3	556	90.6	114	4	US-10-027-725A-7
4	524.5	85.4	121	4	US-10-309-762-152
5	524	85.3	118	4	US-10-309-762-138
6	523.5	85.3	123	4	US-10-309-762-10
7	521	84.9	120	4	US-10-309-762-13
8	521	84.9	120	4	US-10-309-762-144
9	521	84.9	122	4	US-10-309-762-147
10	520	84.7	221	3	US-09-972-656-80
11	519.5	84.6	121	4	US-10-309-762-151
12	519.5	84.6	125	4	US-10-309-762-11
13	518	84.4	121	5	US-10-805-177-56
14	517.5	84.3	119	4	US-10-309-762-140
15	517.5	84.3	148	6	US-11-131-648-13
16	517.5	84.3	148	6	US-11-131-648-35
17	517	84.2	125	5	US-10-805-177-53
18	516.5	84.1	123	4	US-10-309-762-12
19	516.5	84.1	144	5	US-10-893-576-35
20	516	84.0	124	4	US-10-309-762-75
21	516	84.0	143	4	US-10-309-762-96
22	515.5	84.0	117	4	US-10-330-613-13
23	515.5	84.0	117	4	US-10-330-530-13
24	515.5	84.0	117	4	US-10-660-357-13
25	514	83.7	120	4	US-10-309-762-128
26	514	83.7	120	4	US-10-309-762-139
27	514	83.7	121	4	US-10-308-817-137

28	514	83.7	121	4	US-10-453-698-137
29	514	83.7	122	5	US-10-984-960A-56
30	513	83.6	116	4	US-10-309-762-127
31	512.5	83.5	125	4	US-10-309-762-8
32	512.5	83.5	125	4	US-10-309-762-16
33	512.5	83.5	480	5	US-10-910-901-6
34	511.5	83.3	119	4	US-10-309-762-131
35	511.5	83.3	140	5	US-10-893-576-41
36	511	83.2	110	4	US-10-309-762-74
37	510.5	83.1	123	4	US-10-309-762-9
38	510.5	83.1	127	4	US-10-309-762-14
39	510.5	83.1	148	5	US-10-893-576-31
40	509	82.9	149	5	US-10-910-901-22
41	508.5	82.8	123	5	US-10-893-576-190
42	508.5	82.8	125	4	US-10-309-762-153
43	508	82.7	128	5	US-10-727-155-2
44	508	82.7	128	5	US-10-727-155-10
45	508	82.7	128	5	US-10-727-155-30

ALIGNMENTS

RESULT 1
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match 100.0%; Score 614; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LES	G	P	G	L	V	K	P	S	Q	T	L	S	T	C	T	V	S	G	S	I	R	S	G	G	Y	T	W	S	I	R	Q	P	P	G	K	L	E	W	I	G	V	I	H	S	G	N	T	Y	N	P	S	60
Db	1	LES	G	P	G	L	V	K	P	S	Q	T	L	S	T	C	T	V	S	G	S	I	R	S	G	G	Y	T	W	S	I	R	Q	P	P	G	K	L	E	W	I	G	V	I	H	S	G	N	T	Y	N	P	S	60

RESULT 2
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match      97.8%; Score 600; DB 4; Length 114;
Best Local Similarity 96.5%; Pred. No. 2.1e-46;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYHSGNTYNNPS 60
Db 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQGLTVTVSS 114
Db 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYVCARSDGYTLDNWGQGLTVTVSS 114

RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgG-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match      90.6%; Score 556; DB 4; Length 114;
Best Local Similarity 90.4%; Pred. No. 2e-42;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYHSGNTYNNPS 60
Db 1 LESGPGLVKPAQTLSCAVSGGSIRSGGYWWSWIROPKGLWIGYIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQGLTVTVSS 114
Db 61 LKSRITMSVDTSENKFSRLNSVTAADTAVYCARLDGYTLIDWGQGLTVTVSS 114

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152
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Query Match      85.4%; Score 524.5; DB 4; Length 121;
Best Local Similarity 86.2%; Pred. No. 1.4e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYSGSTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSD--GYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCAAYDILTGIAFDINGQGGMVTVSS 121

RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match      85.3%; Score 524; DB 4; Length 118;
Best Local Similarity 88.5%; Pred. No. 1.5e-39;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYHSGNTYNNPSL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGGSIRSGGYWWSWIROPKGLWIGYIYSGSTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYVCARSDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYVCARYYSGSDYWGQGLTVTVSS 118

RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
```

Query Match 85.3%; Score 523.5; DB 4; Length 123;
Best Local Similarity 85.6%; Pred. No. 1.8e-39;
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;
QY 2 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSGDYT-----DGYTLDNWGGTTLVTSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCARAGKYGSGSYLDWGGTTLVTSS 123

RESULT 7
US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13

Query Match 84.9%; Score 521; DB 4; Length 120;
Best Local Similarity 87.1%; Pred. No. 2.9e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
QY 2 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSGDYT-----LDNWGGTTLVTSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCAR-DGYNWYFDLWGRGTLVTSS 120

RESULT 8
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-309-762-144

Query Match 84.9%; Score 521; DB 4; Length 120;
Best Local Similarity 87.1%; Pred. No. 2.9e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
QY 2 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSGDYT-----LDNWGGTTLVTSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCAR-DGYNWYFDLWGRGTLVTSS 120

RESULT 9
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

Query Match 84.9%; Score 521; DB 4; Length 122;
Best Local Similarity 85.5%; Pred. No. 3e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
QY 2 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 61
DB 6 ESGPGLVKPSQTLTCTVSGGSISSGGYYSWIRQHPGKLEWIGYIYHSGNTYINPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYCAR-----SDGYTLDNWGGTTLVTSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYCAR-YDILTGYGMDVWGGTTLVTSS 122

RESULT 10
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Wei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80

Query Match 84.7%; Score 520; DB 3; Length 221;

	Best Local Similarity	86.7%;	Pred. No. 6.6e-39;	Matches	98; Conservative	4; Mismatches	11; Indels	0; Gaps	0;
Qy	2	ESGPGLVKPQSITSLTCTVSGSIRSCGYMSWIRPPGKGLEWIGYIHS	GNTYINPSL	61					
		:							
Db	6	ESGPGLVKPSETLSLTCAVSGGSISGGYSWSWIRPPGKGLEWIGYIHS	GSYINPSL	65					
		:							
Qy	62	KSRVTMSGVDTSKNHFSRLRSVTTAADTAIVVCARSDGYTLDNMGQGLTVTVSS	114						
		:							
Db	66	KSRVTISVDRSKNOFSLKLSSVTAADTAIVVCARGDMGYEDVMCGQLTVTVSS	118						
		:							

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RESULT 11
US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AEGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151

```

	Query Match	84.6%	Score 519.5	DB 4	Length 121
	Best Local Similarity	86.2%	Pred. No. 4e-39		
	Matches 100	Conservative	5	Mismatches 8	Indels 3
				Gaps	1
Qy	2	ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYSWMIROPPGKLEWIGYIYHSGNTYINP	SL	61	
Db	6	ESGPGLVKPSQTLSLTCTVSGGSIRSGGYYSWMIROPPGKLEWIGYIYSGT	YINP	65	
Qy	62	KSRVTMSVDTSKQHFSLRLSSVTAADTAVYYCAR	---	DGYTLDNMQGGTLVT	VS 114
Db	66	KSRVTISVDTSKQFSLRLSSVTAADTAVYYCAR	VLWFGGMDVWGSGT	VT	VS 121

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RESULT 12
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudasz, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11

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	Query Match	84.6%;	Score 519.5;	DB 4;	Length 125;
	Best Local Similarity	83.3%;	Pred. No. 4.1e-39;		
	Matches 100;	Conservative	6;	Mismatches 7;	Indels 7; Gaps 2;
Qy	2	ESGPGIWKPSQTLSTLCTCTVSGSISGGYIYWSWIRPPKGLIEWIGYIYHSGNTYNNPSL	61		
Db	6	ESGPGIWKPSQTLSTLCTCTVSGSISGGYIYWSWIRPPKGLIEWIGYIYHSGNTYNNPSL	65		
Qy	62	KSRVTMSVDTSKNHFGLRLSLSVTAADTAVYICARS-----DGY--TLDNKGQQTLLVTVSS	114		
Db	66	KSRITTSVDTKNQFSLKLSVTAADTAVYICARTYDELDTGYPDAFDLWGQGTMTVTVSS	125		

```

RESULT 13
US-10-805-177-56
; Sequence 56, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Poltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khrantsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-56

```

	Query Match	84.4%;	Score 518;	DB 5;	Length 121;
	Best Local Similarity	84.3%;	Pred. No. 5.5e-39;		
	Matches	97;	Conservative	9;	Mismatches 7; Indels 2; Gaps 1;
Qy	2	ESGPGLVKPSQTL	SLTCTVSGSGISRGGYWISWIRPPGKGLEWIGYIYHSGNTYNNPSL	61	
Db	6	ESGPGLVKPS	ETLSLTCTVSGGSVSGGYWISWIRPPGKGLEWIGYIYSGSTNNPSL	65	
Qy	62	KSRVTMSVDTSKNHF	LSRLSSVTAADTAVYVCARSDGY--TLDNMGQGLVTVVSS	114	
Db	66	KSRVTT SVDTSKN	QFSLKTSSVTAADTAVYVCARNNNNNNNEDYWGQGLVTVVSS	120	

RESULT 14
US-10-309-762-140
; Sequence 140, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX. 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-140

Query Match 84.3%; Score 517.5; DB 4; Length 119;
Best Local Similarity 86.8%; Pred. No. 5.9e-39;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYWMIQPPGKLEWIGYIYHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSLTCTVSGGSISGGYWSMIQHPGKLEWIGYIYHSGNTYNNPSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-GYTLDNWGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGNTYYGMDVWGQGLTVTVSS 119

RESULT 15

US-11-131-648-13
; Sequence 13, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Rid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131.648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-13

Query Match 84.3%; Score 517.5; DB 6; Length 148;
Best Local Similarity 83.5%; Pred. No. 7.4e-39;
Matches 101; Conservative 4; Mismatches 7; Indels 9; Gaps 2;
QY 2 ESGPGLVKPSQTLSLTCTVSGGSIRSGGYWMIQPPGKLEWIGYIYHSGNTYNNPSL 61
DB 15 ESGPGLVKPSQTLSLTCTVSGGSISGGYWSMIQHPGKLEWIGYIYHSGNTYNNPSL 74
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDG-----YTLDNWGQGLTVTVS 113
DB 75 KSRVTMSVDTSKNQFSLKLSVTAADTAVYYCAR-DGITMIRGYYGMDVWGQGLTVTVS 133
QY 114 S 114
DB 134 S 134

Search completed: April 3, 2006, 15:20:23
Job time : 78.9 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:13:12 ; Search time 10.3636 Seconds
(without alignments)
334.861 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614

Sequence: 1 LESGGLVPSQTLSTCTV.....RSDGYTLDNWGQGLTVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SID55/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SID55/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SID55/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 5: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 6: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 7: /SID55/ptodata/1/pubpaa/US12 NEW PUB.pap.*
- 8: /SID55/ptodata/1/pubpaa/US13 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	82.7	172	7	US-11-128-900-7
2	508	82.7	172	7	US-11-128-900-86
3	507	82.6	252	7	US-11-054-515-1994
4	507	82.6	252	7	US-11-266-444-1994
5	506.5	82.5	253	7	US-11-054-515-1619
6	506.5	82.5	253	7	US-11-266-444-1619
7	503	81.9	252	7	US-11-054-515-1329
8	503	81.9	252	7	US-11-266-444-1329
9	502.5	81.8	119	6	US-10-834-397-39
10	502.5	81.8	119	6	US-10-834-397-65
11	501	81.6	256	7	US-11-054-515-1607
12	501	81.6	256	7	US-11-266-444-1607
13	494.5	80.5	251	7	US-11-054-515-990
14	494.5	80.5	251	7	US-11-266-444-990
15	491	80.0	118	6	US-10-834-397-25
16	489	79.6	116	7	US-11-102-424-5
17	487.5	79.4	119	6	US-10-530-171-7
18	485	79.0	254	7	US-11-054-515-1578
19	485	79.0	254	7	US-11-266-444-1578
20	484	78.8	146	6	US-10-721-763-17
21	483	78.7	256	7	US-11-054-515-1745
22	483	78.7	256	7	US-11-266-444-1745
23	482	78.5	154	6	US-10-721-763-25
24	482	78.5	250	7	US-11-054-515-1548
25	482	78.5	250	7	US-11-266-444-1548

26	479.5	78.1	117	7	US-11-012-353-162	Sequence 162, Appl
27	478	77.9	116	7	US-11-102-424-6	Sequence 6, Appl
28	476	77.5	240	6	US-10-902-546-12	Sequence 12, Appl
29	475.5	77.4	468	7	US-11-086-289-14	Sequence 14, Appl
30	475	77.4	247	7	US-11-054-515-1651	Sequence 1651, Ap
31	475	77.4	247	7	US-11-266-444-1651	Sequence 1651, Ap
32	474.5	77.3	113	7	US-11-144-248-20	Sequence 20, Appl
33	474.5	77.3	113	7	US-11-144-222-20	Sequence 20, Appl
34	474.5	77.3	113	7	US-11-182-343-20	Sequence 20, Appl
35	474	77.2	116	7	US-11-102-424-10	Sequence 10, Appl
36	474	77.2	116	7	US-11-102-424-11	Sequence 11, Appl
37	474	77.2	248	7	US-11-054-515-1360	Sequence 1360, Ap
38	474	77.2	248	7	US-11-266-444-1360	Sequence 1360, Ap
39	473	77.0	252	7	US-11-054-515-1401	Sequence 1401, Ap
40	473	77.0	252	7	US-11-266-444-1401	Sequence 1401, Ap
41	472	76.9	277	6	US-10-996-007B-13	Sequence 13, Appl
42	472	76.9	277	6	US-10-996-007B-14	Sequence 14, Appl
43	471.5	76.8	123	7	US-11-012-353-73	Sequence 73, Appl
44	470	76.5	116	7	US-11-102-424-13	Sequence 13, Appl
45	469	76.4	99	7	US-11-054-669-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-11-128-900-7
; Sequence 7, Application US/11128900
; Publication NO. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: CARVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-7

Qy	3	SGPGLVPSQTLSTCTVSGGIRSGGYWGWIRQPPGKGLGWIGYIYHSGNTYNSLK 62
Db	1	SGPGLVPSQTLSTCTVSGGIRSGGYWGWIRQPPGKGLGWIGYIYHSGNTYNSLK 60
Qy	63	SRVTMSVDTSKNHFSLRLSSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114
Db	61	SRVTISVDTSKNQSLKLSVTAADTAVYCARSDG--YTLDNWGQGLTVTVSS 114

RESULT 2
US-11-128-900-86
; Sequence 86, Application US/11128900


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; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1619
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1619

Query Match      82.5%; Score 506.5; DB 7; Length 253;
Best Local Similarity 81.1%; Pred. No. 3.2e-36;
Matches 99; Conservative 6; Mismatches 8; Indels 9; Gaps 2;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----DGYT--LDNWGQGLTVTV 112
Db 66 KSRVTISIDTSKNQFSLKLSVTAADTAVYYCVRSYDILTGRPYTDAFDWKGGLTVTV 125

Qy 113 SS 114
Db 126 SS 127

RESULT 6
US-11-266-444-1619
; Sequence 1619, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulato
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 3239
; SEQ ID NO 1619
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-11-266-444-1619

Query Match      82.5%; Score 506.5; DB 7; Length 253;
Best Local Similarity 81.1%; Pred. No. 3.2e-36;
Matches 99; Conservative 6; Mismatches 8; Indels 9; Gaps 2;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----DGYT--LDNWGQGLTVTV 112
Db 66 KSRVTISIDTSKNQFSLKLSVTAADTAVYYCVRSYDILTGRPYTDAFDWKGGLTVTV 125

Qy 113 SS 114
Db 126 SS 127

RESULT 7
US-11-054-515-1329
; Sequence 1329, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1329
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1329

Query Match      81.9%; Score 503; DB 7; Length 252;
Best Local Similarity 81.0%; Pred. No. 6.3e-36;
Matches 98; Conservative 6; Mismatches 9; Indels 8; Gaps 2;

Qy 2  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 61
Db 6  ESGPGLVKPSQTLSLTCTVSGGSIIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYYPNPSL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSD-----GYTL---DNWGQGLTVTVS 113
Db 66 KSRVTISIDTSKNQFSLKLSVTAADTAVYYCARGDYDILATGYPLHAFDINGKGLTVTVS 125

Qy 114 S 114
Db 126 S 126

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RESULT 8
US-11-266-444-1329
; Sequence 1329, Application US/11266444
; Publication No. US20060062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulat
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-1329

Query Match      81.8%; Score 503; DB 7; Length 252;
Best Local Similarity 81.0%; Pred. No. 6.3e-36;
Matches 98; Conservative 6; Mismatches 9; Indels 8; Gaps 2;

Qy      2  ESGPGLVKPSQTLSTCTVSGGSIKNSVTAADTAVYICARSD-----GYTL----DNWGQGLTVTVS 113
Db      6  ESGPGLVKPSQTLSTCTVSGGSIKNSVTAADTAVYICARSD-----GYTL----DNWGQGLTVTVS 125

Qy      62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSD-----GYTL----DNWGQGLTVTVS 113
Db      66  KSRVTISVDTSKNQFSLKLSVTAADTAVYICARGDYDILTGYPLHAFDIWKGKTLTVTS 125

Qy      114 S 114
Db      126 S 126

RESULT 9
US-10-834-397-39
; Sequence 39, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

US-10-834-397-39
; Sequence 39, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-834-397-39

Query Match      81.8%; Score 502.5; DB 6; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.5e-36;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy      2  ESGPGLVKPSQTLSTCTVSGGSIKNSVTAADTAVYICARSD-----SDG-YTLDNWGQGLTVTVSS 61
Db      6  ESGPGLVKPSQTLSTCTVSGGSIKNSVTAADTAVYICARSD-----SDG-YTLDNWGQGLTVTVSS 63

Qy      62  KSRVTMSVDTSKNHFSLRLSSVTAADTAVYICARSD-----SDG-YTLDNWGQGLTVTVSS 114
Db      64  KSRVTISVDTSKNQFSLKLSVTAADTAVYICARSD-----SDG-YTLDNWGQGLTVTVSS 119

RESULT 10
US-10-834-397-65
; Sequence 65, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

US-10-834-397-65
; Sequence 65, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

US-10-834-397-65
; Sequence 65, Application US/10834397
; Publication No. US2006003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
```

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-834-397-65

Query Match 81.6%; Score 502.5; DB 6; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.5e-36;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;
QY 2 ESGPGLVKPSQTLSTCTVSGGSISSGGYVWSWIRQPPGKLEWIGYVHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSISS--YVWSWIRQPPGKLEWIGYVHSGNTYNP 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCAR--SDG-YTLDNWGGTGLTV 114
DB 64 KSRVTISVDTSKNQFSLKLSSTVTAADTAVVYCARWGGDGFYANDYWGQGLTVTV 119

RESULT 11
US-11-054-515-1607
Sequence 1607, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS

FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1607
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1607

Query Match 81.6%; Score 501; DB 7; Length 256;
Best Local Similarity 77.6%; Pred. No. 9.5e-36;
Matches 97; Conservative 4; Mismatches 12; Indels 12; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSISSGGYVWSWIRQPPGKLEWIGYVHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSISSGGYVWSWIRQPPGKLEWIGYVHSGNTYNP 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD-----GYTLDNWGGTGL 109
DB 66 KSRVTISVDRSKNQFSLKLSSTVTAADTAVVYCARQKRGDYDILTYQLGYAFDIWGRGTP 125
QY 110 VTSS 114
DB 126 VTSS 130

RESULT 12
US-11-266-444-1607
Sequence 1607, Application US/11266444
Publication No. US20060062789A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulator
FILE REFERENCE: PF523P1D1
CURRENT APPLICATION NUMBER: US/11/266,444
CURRENT FILING DATE: 2005-11-04
PRIOR APPLICATION NUMBER: 09/880,746
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1607
LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
US-11-266-444-1607

Query Match 81.6%; Score 501; DB 7; Length 256;
Best Local Similarity 77.6%; Pred. No. 9.5e-36;
Matches 97; Conservative 4; Mismatches 12; Indels 12; Gaps 1;
QY 2 ESGPGLVKPSQTLSTCTVSGGSISSGGYVWSWIRQPPGKLEWIGYVHSGNTYNP 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSISSGGYVWSWIRQPPGKLEWIGYVHSGNTYNP 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVVYCARSD-----GYTLDNWGGTGL 109
DB 66 KSRVTISVDRSKNQFSLKLSSTVTAADTAVVYCARQKRGDYDILTYQLGYAFDIWGRGTP 125
QY 110 VTSS 114
DB 126 VTSS 130

RESULT 13
US-11-054-515-990
Sequence 990, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347

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; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 990
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-990

Query Match      80.5%; Score 494.5; DB 7; Length 251;
Best Local Similarity 79.2%; Pred. No. 3.3e-35;
Matches 95; Conservative 8; Mismatches 10; Indels 7; Gaps 1;

Qy  2  ESGPGLVKPSQTLSTCTVSGGSGIRGGYVWSMIROPPGKGLGWIGYIYHSGNTYINPSL 61
Db  6  ESGPGLVKPSETLSLTCTVSGGSISSSSYYGWIROPPGKGLGWIGSIYSGSTYINPSL 65
Qy  62  KSRVTWSVDTSKNHFSRLSSVTAADTAVYYCAR-----SDGYTLDNWGQGLVTVSS 114
Db  66  KSRVTISVDTSKNQFSLKLSVTAADTAVYYCARFYDILTSTYYGMDVWGRGTMTVTVSS 125

RESULT 14
US-11-266-444-990
; Sequence 990, Application US/11266444
; Publication No. US2006062789A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulated
; FILE REFERENCE: PF523P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 990
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-266-444-990

Query Match      80.5%; Score 494.5; DB 7; Length 251;
Best Local Similarity 79.2%; Pred. No. 3.3e-35;
Matches 95; Conservative 8; Mismatches 10; Indels 7; Gaps 1;

Qy  2  ESGPGLVKPSQTLSTCTVSGGSGIRGGYVWSMIROPPGKGLGWIGYIYHSGNTYINPSL 61

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Search completed: April 3, 2006, 15:21:29
Job time : 11.3636 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:09 ; Search time 92.1879 Seconds
(without alignments)
505.209 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELQSPSSLSASVGDRTVIS.....QESLSASYTFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533	98.2	106	ABG30448	Abg30448 Human IgE
2	475	87.5	107	AAR54260	Aar54260 Anti-HIV
3	475	87.5	107	AAW01283	AAW01283 VL region
4	475	87.5	107	AAy98244	AAy98244 Anti-gp12
5	475	87.5	107	AAy95135	AAy95135 Anti-gp12
6	474	87.3	107	AAG93667	Aag93667 Human ant
7	474	87.3	107	ABO27474	ABO27474 Anti-Rh(D
8	472	86.9	107	AAG93663	Aag93663 Human ant
9	472	86.9	107	AAG93664	Aag93664 Human ant
10	472	86.9	107	AAG93590	Aag93590 Human ant
11	472	86.9	107	ABO27471	ABO27471 Anti-Rh(D
12	472	86.9	107	ABO27397	ABO27397 Anti-Rh(D
13	472	86.9	107	ABO27470	ABO27470 Anti-Rh(D
14	471	86.7	107	AAG93644	Aag93644 Human ant
15	471	86.7	107	ABO27451	ABO27451 Anti-Rh(D
16	468	86.2	106	ADx01785	Adx01785 SARS coro
17	468	86.2	107	AAG93593	Aag93593 Human ant
18	468	86.2	107	ABO27400	ABO27400 Anti-Rh(D
19	468	86.2	116	ADW04873	Adw04873 PAPP-A im
20	468	86.2	240	AEb46929	Aeb46929 Human CD1
21	468	86.2	240	AEb46937	Aeb46937 Human CD1
22	468	86.2	240	AEb46939	Aeb46939 Human CD1
23	468	86.2	241	AEb46931	Aeb46931 Human CD1
24	468	86.2	243	ADW90303	Adw90303 Phage scF

25	468	86.2	243	9	ADx01791	Adx01791 SARS coro
26	468	86.2	244	8	ADH34565	Adh34565 scFv SC02
27	468	86.2	244	8	ADR23318	Adr23318 Human CD7
28	468	86.2	244	8	ADR23330	Adr23330 Human CD7
29	468	86.2	244	8	ADR23332	Adr23332 Human CD7
30	468	86.2	244	9	ADW11304	Adw11304 Human C-t
31	468	86.2	244	9	ADW11306	Adw11306 Human C-t
32	468	86.2	245	8	ADR23320	Adr23320 Human CD7
33	468	86.2	245	8	ADR23320	Adr23320 Phage scF
34	468	86.2	245	9	ADW90309	Adw90309 Phage scF
35	468	86.2	245	9	ADW90311	Adw90311 Phage scF
36	468	86.2	245	9	ADW90306	Adw90306 Phage scF
37	468	86.2	245	9	ADW90305	Adw90305 Phage scF
38	468	86.2	245	9	ADW90305	Adw90305 Phage scF
39	468	86.2	245	9	ADW90305	Adw90305 Phage scF
40	468	86.2	245	9	ADW90316	Adw90316 Phage scF
41	468	86.2	247	9	ADW90316	Adw90316 Phage scF
42	468	86.2	247	9	ADW90308	Adw90308 Phage scF
43	468	86.2	247	9	ADW90308	Adw90308 Phage scF
44	468	86.2	247	9	ADx01840	Adx01840 SARS coro
45	468	86.2	248	9	ADx01801	Adx01801 SARS coro
					ADW90310	Phage scF

ALIGNMENTS

RESULT 1

ABG30448

ID ABG30448 standard; protein; 106 AA.

XX AC

ABG30448;

DT 21-OCT-2002 (first entry)

XX Human IgE Fab clone 94 light chain protein.

XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;

XX timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21

FT Region /note= "FR1 region"

FT Region 22..32

FT Region /note= "CDR1 region"

FT Region 33..47

FT Region /note= "FR2 region"

FT Region 48..54

FT Region /note= "CDR2 protein"

FT Region 55..86

FT Region /note= "FR3 region"

FT Region 87..95

FT Region /note= "CDR2 region"

FT Region 96..104

FT Region /note= "FR4 region"

XX WO200253595-A1.

XX 11-JUL-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX PI Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX N-PSDB; ASK89640.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising

PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.

XX
XX Disclosure; Page 39; 45pp; English.

PS This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergen patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC fab, clone 94 light chain protein of the invention
XX
SQ Sequence 106 AA;

Query Match 98.2%; Score 533; DB 5; Length 106;
Best Local Similarity 99.1%; Pred. No. 5.3e-33;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SGSGYGTDFLTITSSSQFEDFASYYCOESLSASVTFQGTQKVEIKR 106
Db 61 SGSGYGTDFLTITSSSQFEDFASYYCOESLSASVTFQGTQKVEIKR 106

RESULT 2
AAR54260
ID AAR54260 standard; protein; 107 AA.

XX AAR54260;

XX 25-MAR-2003 (revised)

DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b22.

XX Human immunodeficiency virus: HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..21 /label= FR1
FT Region	22..33 /label= CDR1
FT Region	34..48 /label= FR2
FT Region	49..55 /label= CDR2
FT Region	56..87 /label= FR3
FT Region	88..95 /label= CDR3
FT Region	96..107 /label= FR4

XX WO9407922-A1.

PD 14-APR-1994.

XX 30-SEP-1993; 93WO-US009328.
PF
XX 30-SEP-1992; 92US-00954148.
PR
XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 1994-135516/16.

XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.

PS Claim 5; Page 189; 248pp; English.

XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAb regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54260
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 107 AA;

Query Match 87.5%; Score 475; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SGSGYGTDFLTITSSSQFEDFASYYCOESLSASVTFQGTQKVEIKR 106
Db 61 SGSGYGTDFLTITSSSQFEDFATYYCQSYSTPTTFQGTQKLEIKR 106

RESULT 3

AAW01283

ID AAW01283 standard; protein; 107 AA.

XX AAW01283;

XX 29-JAN-1997 (first entry)

XX VL region of HIV neutralising MAb, clone b22 and B35.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.

XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..21 /label= FR1
FT Region	22..32 /label= CDR1
FT Region	33..47 /label= FR2
FT Region	48..54 /label= CDR2
FT Region	55..86 /label= FR3
FT Region	87..95 /label= CDR3
FT Region	96..107 /label= FR4

XX WO9602273-A1.
 XX 01-FEB-1996.
 XX 11-JUL-1995; 95WO-US008743.
 XX 18-JUL-1994; 94US-00276852.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI; 1996-179601/18.
 XX Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
 XX immuno:therapy and detection of HIV infection.
 XX Example; Fig 11; 366pp; English.
 XX The sequences given in AA01261-92 represent the light chain variable
 XX regions (VL) of a series of monoclonal antibodies (Mab's) which are
 XX immunoreactive with HIV glycoprotein gp120 and are capable of
 XX neutralising HIV. This sequence represents the sequence of the JK2 gene
 XX clones, b22 and B35. A Mab containing this VL sequence has the capacity
 XX to reduce HIV infectivity titre in an in vivo virus infectivity assay by
 XX 50 % at a concentration of less than 700 ng of antibody/ml, and binds
 XX mature gp120 preferentially over the precursor gp160. The Mab may be used
 XX for determining immunocompetence of a human anti-HIV antibody and in the
 XX detection of HIV infection
 XX SQ Sequence 107 AA;
 Query Match 87.5%; Score 475; DB 2; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.3e-28;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITICRASQRIYNTYQHPKAPKLLIYAASSLSQGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60
 QY 61 SGSGYGTDFLTITSSLPEDFASYCQESLSASVTFGGTKVEIKR 106
 DB 61 SGSGSGTDFLTITSSLPEDFATYCCQSYSTPTTFGGTKLEIKR 106
 RESULT 4
 AAY98244
 ID AAY98244 standard; protein; 107 AA.
 XX AAY98244;
 XX 04-JUL-2000 (first entry)
 XX Anti-gp120 antibody light chain variable region from clone b22.
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 XX human immunodeficiency virus type 1; HIV-1; infectivity titre;
 XX passive immunotherapy; reduce severity; HIV-induced disease;
 XX immunocompetence; active immunisation.
 XX Homo sapiens.
 XX AU9948754-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048754.
 XX 16-SEP-1999; 99AU-00048754.
 XX (SCRI) SCRIPPS RES INST.
 XX

PI Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-246867/22.
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 XX (HIV) used for providing passive immunotherapy to HIV are specific for
 XX glycoprotein-120.
 XX Example 9; Fig 11; 374pp; English.
 XX This sequence represents a fragment of the antibodies of the invention.
 XX The invention relates to the production of an anti-HIV (human
 XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 XX of reducing an HIV infectivity titre in an in vitro virus infectivity
 XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
 XX production of the antibody comprises: (a) providing a first
 XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 XX (which does not comprise the sequence represented by AAY98206) and a
 XX second polynucleotide encoding a light chain immunoglobulin amino acid
 XX sequence; (b) inserting the first and second polynucleotide sequences
 XX into a host cell; (c) maintaining the host cell in conditions which allow
 XX the amino acid sequences encoded by the polynucleotides to be expressed
 XX in the host cell; and (d) isolating the antibody comprising the heavy and
 XX light chain immunoglobulin amino acid sequences from the host cell. The
 XX anti-HIV gp-120 monoclonal antibody is used for providing passive
 XX immunotherapy to HIV in a human. They can be administered to high-risk
 XX patients to reduce the likelihood and/or severity of HIV-induced disease
 XX and to patients who are already HIV-infected. The antibodies are used for
 XX neutralising field isolates which provides information about the
 XX immunocompetence of an immune response in HIV patients, for detecting HIV
 XX in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 XX producing anti-idiotypic antibodies which can be used for active
 XX immunisation and to screen human monoclonal antibodies to identify those
 XX with the same binding specificity and to monitor the course of HIV
 XX disease therapy by measuring the changes in concentration of HIV present
 XX in the body or in body fluids by immunoassay. The anti-HIV gp-120
 XX monoclonal antibodies are encoded by a human polynucleotide sequence and
 XX when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 XX reduce the problems of significant host immune response to the antibodies
 XX associated with monoclonal antibodies of xenogeneic or chimeric
 XX derivation
 XX SQ Sequence 107 AA;
 Query Match 87.5%; Score 475; DB 3; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.3e-28;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITICRASQRIYNTYQHPKAPKLLIYAASSLSQGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPKAPKLLIYAASSLSQGVPSRF 60
 QY 61 SGSGYGTDFLTITSSLPEDFASYCQESLSASVTFGGTKVEIKR 106
 DB 61 SGSGSGTDFLTITSSLPEDFATYCCQSYSTPTTFGGTKLEIKR 106
 RESULT 5
 AAY95135
 ID AAY95135 standard; protein; 107 AA.
 XX AAY95135;
 XX 30-JUN-2000 (first entry)
 XX Anti-gp120 antibody light chain variable region from clone b22.
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 XX reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 XX glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX Homo sapiens.
 XX

PN AU9948756-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048756.
 PF 16-SEP-1999; 99AU-00048756.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 PI WPI; 2000-293393/26.
 XX Novel human monoclonal antibodies which immunoreact with and neutralize
 PT human immunodeficiency virus useful for treating HIV infections.
 XX
 XX Example 9; Fig 11; 366pp; English.
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotides sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 XX Sequence 107 AA;
 SQ
 Query Match 87.5%; Score 475; DB 3; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.3e-28;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
 QY 61 SGSGYGTDFLTITSSLOQFEDFASYCQESLSASVTFQGTKEIKR 106
 DB 61 SGSGSGTDFLTITSSLOQFEDFATYYCQSYSTPTFTFQGTKEIKR 106
 RESULT 6
 ID AAG93667
 AC AAG93667 standard; protein; 107 AA.
 AC AAG93667;
 XX 14-SEP-2001 (first entry)
 DT Human anti-Rh(D) antibody clone SH54 protein sequence.
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 PF

XX Homo sapiens.
 OS US6255455-B1.
 PN 03-JUL-2001.
 XX 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 XX 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 XX N-PSDB; AAH68724.
 DR New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Claim 1; Col 70; 162pp; English.
 PS The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX Sequence 107 AA;
 SQ
 Query Match 87.3%; Score 474; DB 4; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.5e-28;
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
 DB 2 ELTQSPSSLSASVGDRTVITSCRASQSIYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
 QY 61 SGSGYGTDFLTITSSLOQFEDFASYCQESLSASVTFQGTKEIKR 106
 DB 62 SGSGSGTDFLTITSSLOQFEDFATYYCQSYSTPTFTFQGTKEIKR 107
 RESULT 7
 ID ABO27474
 XX ABO27474 standard; protein; 107 AA.
 AC ABO27474;
 XX 12-SEP-2003 (first entry)
 DT Anti-Rh(D) light chain SH54.
 DE Human; RH(D) binding protein; blood typing; blood product; antibody;
 XX magnetically activated cell sorting.
 KW Homo sapiens.
 OS US2003040605-A1.
 PN 27-FEB-2003.
 PD 04-MAY-2001; 2001US-00848798.
 PF

XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 XX WPI; 2003-512273/48.
 DR N-PSDB; ACD45388.
 XX New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX Claim 4; Page 53; 187pp; English.
 XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents the amino acid sequence of a human anti-Rh(D) chain
 XX Sequence 107 AA;
 SQ
 Query Match 87.3%; Score 474; DB 6; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.5e-28;
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
 DB 2 ELTQSPSSMSASVGDRTVITICRASQSIGTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
 QY 61 SGSGYGTDFLTITISLQDFEFASYCQESLSASYTFQGTQKVEIKR 106
 DB 62 SGSGSGTDFLTITISLQDFEFATYCCQSYSTPTWTFQGTQKVEIKR 107
 RESULT 8
 AAG93663
 ID AAG93663 standard; protein; 107 AA.
 XX AAG93663;
 AC
 XX 14-SEP-2001 (first entry)
 DT Human anti-Rh(D) antibody clone SH49 protein sequence.
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX red blood cell; Rh phenotype; diagnosis; therapeutic.
 KW Homo sapiens.
 OS US6255455-B1.
 XX 03-JUL-2001.
 PD 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 XX WPI; 2001-388931/41.
 DR N-PSDB; AAH68720.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in

PT therapeutic medicine.
 XX Claim 1; Col 69; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX Sequence 107 AA;
 SQ
 Query Match 86.9%; Score 472; DB 4; Length 107;
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
 DB 2 ELTQSPSSLSASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
 QY 61 SGSGYGTDFLTITISLQDFEFASYCQESLSASYTFQGTQKVEIKR 106
 DB 62 SGSGSGTDFLTITISLQDFEFATYCCQSYSTPTWTFQGTQKVEIKR 107
 RESULT 9
 AAG93664
 ID AAG93664 standard; protein; 107 AA.
 XX AAG93664;
 AC
 XX 14-SEP-2001 (first entry)
 DT Human anti-Rh(D) antibody clone SH50 protein sequence.
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX red blood cell; Rh phenotype; diagnosis; therapeutic.
 KW Homo sapiens.
 OS US6255455-B1.
 XX 03-JUL-2001.
 PD 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 XX WPI; 2001-388931/41.
 DR N-PSDB; AAH68721.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 CC therapeutic medicine.
 XX Claim 1; Col 69; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention

XX SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.2e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGYGTDTLTITSSIQFEDFASVYQESLSASVYTFGQGTKEIKR 106
DB 62 SSGSGYGTDTLTITSSIQFEDFATYVYQESYSTPTWTFGQGTKEIKR 107

RESULT 10

AA93590
ID AAG93590 standard; protein; 107 AA.

AC AAG93590;

XX 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain I02 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.

XX Homo sapiens.

XX US625455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2001-388931/41.

XX N-PSDB; AAH68647.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.

XX Claim 1; Col 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH6815 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention

SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.2e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGTDTLTITSSIQFEDFASVYQESLSASVYTFGQGTKEIKR 106
DB 62 SSGSGYGTDTLTITSSIQFEDFATYVYQESYSTPTWTFGQGTKEIKR 107

RESULT 11

ABO27471
ID ABO27471 standard; protein; 107 AA.

XX ABO27471;

XX 12-SEP-2003 (first entry)

XX Anti-Rh(D) light chain SH50.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;
XX magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX 29-JAN-1999; 99US-00240274.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2003-512273/48.

XX N-PSDB; ACD45385.

XX New human Rh(D)-binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 52; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein
XX can be used for magnetically activated cell sorting. The protein is
XX useful in various diagnostic and therapeutic applications in humans,
XX including typing of blood or blood products. The present sequence
XX represents the amino acid sequence of a human anti-Rh(D) chain

XX SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.2e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGYGTDTLTITSSIQFEDFASVYQESLSASVYTFGQGTKEIKR 106
DB 62 SSGSGYGTDTLTITSSIQFEDFATYVYQESYSTPTWTFGQGTKEIKR 107

[illegible]

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:27:40 ; Search time 15.097 Seconds
(without alignments)
675.565 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464	85.5	127	2 S40367	Ig kappa chain V-J
2	459	84.5	123	2 S40331	Ig kappa chain - h
3	458	84.3	108	2 B49047	Ig kappa chain V r
4	456	84.0	108	2 S47182	Ig kappa chain - h
5	452	83.2	109	2 S31998	Ig kappa chain - h
6	452	83.2	109	2 S31979	Ig kappa chain - h
7	448	82.5	109	2 S31980	Ig kappa chain - h
8	446	82.1	108	2 S41122	Ig kappa chain V r
9	445	82.0	109	2 S32001	Ig kappa chain - h
10	441	81.2	108	2 S19674	Ig kappa chain V r
11	439	80.8	109	2 S31981	Ig kappa chain - h
12	439	80.8	129	2 S52793	Ig kappa chain V r
13	438	80.7	107	2 S36264	Ig lambda chain V
14	437	80.5	108	2 S31977	Ig kappa chain - h
15	436	80.3	109	2 S31983	Ig kappa chain - h
16	436	80.3	122	2 S40370	Ig kappa chain - h
17	436	80.3	129	1 K1HUWK	Ig kappa chain pre
18	436	80.3	129	2 S40317	Ig kappa chain - h
19	435	80.1	128	2 S46372	Ig light chain var
20	434	79.9	120	2 S46370	Ig kappa chain V-J
21	433.5	79.8	125	2 S40315	Ig kappa chain - h
22	433	79.7	108	1 K1HUDE	Ig kappa chain V-I
23	432	79.6	132	2 S40334	Ig kappa chain - h
24	431	79.4	109	2 S31978	Ig kappa chain - h
25	430	79.2	108	1 K1HUHU	Ig kappa chain V-I
26	430	79.2	132	2 S38646	Ig kappa chain V r
27	425	78.3	122	2 S40314	Ig kappa chain - h
28	425	78.3	129	2 S40369	Ig kappa chain - h
29	424.5	78.2	106	2 PC2397	anti-tetanus toxin

30	423.5	78.0	124	2 S40336	Ig kappa chain V-J
31	422.5	77.8	107	2 S36275	Ig lambda chain V
32	422	77.7	125	2 S40333	Ig kappa chain V-J
33	422	77.7	131	2 S40352	Ig kappa chain V-J
34	420	77.3	108	1 K1HUOU	Ig kappa chain V-I
35	420	77.3	125	2 S40349	Ig kappa chain V-J
36	420	77.3	126	2 S40335	Ig kappa chain V-J
37	419	77.2	125	2 S40350	Ig kappa chain - h
38	418	77.0	117	2 S46371	Ig kappa chain V-J
39	418	77.0	129	2 S52792	Ig kappa chain V r
40	417	76.8	117	2 S46376	Ig kappa chain V-I
41	416	76.6	108	1 K1HUHU	Ig kappa chain V-I
42	414	76.2	107	2 JLO139	Ig kappa chain V r
43	414	76.2	107	2 S36262	Ig kappa chain V
44	414	76.2	108	1 K1HUKA	Ig kappa chain V-I
45	413.5	76.2	108	2 S30521	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40367

Ig kappa chain V-J-C region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40367

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40367

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-127 <KLE>

A;Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 464; DB 2; Length 127;

Best Local Similarity 84.9%; Pred. No. 2.6e-34;

Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVISCRASQINTYINWYQHPGKAPKLLIYAASSLQSGVPSRF 60

Db 20 QMTQSPSSLSASVGDRTVITCRASQISINLYNWYQHPGKAPKLLIYAASSLQSGVPSRF 79

Qy 61 SGSGYGDTFTLTSSLOFEDFASYCOESLSASVTFGGTKVEIKR 106

Db 80 SGSGGTDFTLTSSLOFEDFATYCCQSVNTPTWTFGGTKVEIKR 125

RESULT 2

S40331

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40331

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40331

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-123 <KLE>

A;Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PII

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 459; DB 2; Length 123;

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Best Local Similarity 85.7%; Pred. No. 7e-34; Mismatches 7; Indels 8; Gaps 0;
Matches 90; Conservative

Qy 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHPGKAPKLLIYAASLSQGVPSRF 60
Db 19 QMTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPGKAPKLLIYAASLSQGVPSRF 78

Qy 61 SGSGYGTDFLTITSSLPEDFASVYCOESLSASVTFGGTKVEIKR 105
Db 79 SGSGGTDFLTITSSLPEDFATVYCOQSYSTRTFGGTKVEIKR 123

RESULT 3
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 458; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 7.6e-34; Mismatches 7; Indels 9; Gaps 0;
Matches 90; Conservative

Qy 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHPGKAPKLLIYAASLSQGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPGKAPKLLIYAASLSQGVPSRF 62

Qy 61 SGSGYGTDFLTITSSLPEDFASVYCOESLSASVTFGGTKVEIKR 106
Db 63 SGSGGTDFLTITSSLPEDFATVYCOQSYSTPLTFGGTKVEIKR 108

RESULT 4
S47182
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47182
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
A;Cross-references: UNIPARC:UPI00001161E5; EMBL:X79786; NID:9506422; PIDN:CAA56182.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.1e-33; Mismatches 7; Indels 9; Gaps 0;
Matches 90; Conservative

Qy 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHPGKAPKLLIYAASLSQGVPSRF 60
Db 3 ELTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPGKAPKLLIYAASLSQGVPSRF 62

Qy 61 SGSGYGTDFLTITSSLPEDFASVYCOESLSASVTFGGTKVEIKR 106
```

```
Db 63 SGSGGTDFLTITSSLPEDFATVYCOQSYSTPITSGGTLEIKR 108

RESULT 5
S31978
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31978
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31978
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:938501; PIDN:CAA78790.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;
Best Local Similarity 83.8%; Pred. No. 2.6e-33; Mismatches 7; Indels 9; Gaps 0;
Matches 88; Conservative

Qy 2 LTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHPGKAPKLLIYAASLSQGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPGKAPKLLIYAASLSQGVPSRF 63

Qy 62 GSGYGTDFLTITSSLPEDFASVYCOESLSASVTFGGTKVEIKR 106
Db 64 GSGGTDFLTITSSLPEDFATVYCOQSYSTPITFGHTKVEIKR 108

RESULT 6
S31979
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31979
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31979
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116492; EMBL:Z15075; NID:938489; PIDN:CAA78784.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;
Best Local Similarity 81.9%; Pred. No. 2.6e-33; Mismatches 10; Indels 9; Gaps 0;
Matches 86; Conservative

Qy 2 LTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHPGKAPKLLIYAASLSQGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITICRASQSISSYLNWYQHPGKAPKLLIYAASLSQGVPSRF 63

Qy 62 GSGYGTDFLTITSSLPEDFASVYCOESLSASVTFGGTKVEIKR 106
Db 64 GSGGTDFLTITSSLPEDFATVYCOQSYSTPITFGGTLEIKR 108

RESULT 7
S31980
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
```


C;Accession: S31980; S32000
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31980
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116493; EMBL:Z15076; NID:G38491; PIDN:CAA78785.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 448; DB 2; Length 109;
Best Local Similarity 81.0%; Pred. No. 5.9e-33;
Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYGTSTLQSGVPSRFS 63

Qy 62 GSGYGTDTLTITSSLOPEDFASYCQESLSASVTFGQGTKEIKR 106
Db 64 GSGFGDTLTITSSLOPEDFATYFCQSYSSPYTFGQGTKEIKR 108

RESULT 8
S41122
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44122
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable
A;Reference number: S44105
A;Accession: S44122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
A;Cross-references: UNIPARC:UPI0000116630; EMBL:Z31390; NID:G472976; PIDN:CAAB3265.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 446; DB 2; Length 108;
Best Local Similarity 83.0%; Pred. No. 8.7e-33;
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYASASSLSQSGVPSRF 62

Qy 61 SGSGYGTDTLTITSSLOPEDFASYCQESLSASVTFGQGTKEIKR 106
Db 63 SGSGYGTDTLTITSSLOPEDFATYFCQSYSSPYTFGQGTKEIKR 108

RESULT 9
S32001
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32001
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S32001
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>

A;Cross-references: UNIPARC:UPI0000116498; EMBL:Z15082; NID:G38503; PIDN:CAA78791.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 445; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.1e-32;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYGTSTLQSGVPSRFS 63

Qy 62 GSGYGTDTLTITSSLOPEDFASYCQESLSASVTFGQGTKEIKR 106
Db 64 GSGFGDTLTITSSLOPEDFATYFCQSYSSPYTFGQGTKEIKR 108

RESULT 10
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19674
A;Molecule type: mRNA
A;Residues: 1-108 <UNAR>
A;Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 441; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 2.4e-32;
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRFS 61
Db 4 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRFS 63

Qy 62 GSGYGTDTLTITSSLOPEDFASYCQESLSASVTFGQGTKEIKR 106
Db 64 GSGFGDTLTITSSLOPEDFATYFCQSYSSPYTFGQGTKEIKR 108

RESULT 11
S31981
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31981
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31981
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: UNIPARC:UPI0000116494; EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 3.7e-32;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRFS 61

[illegible]

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:37 ; Search time 89.6182 Seconds
(without alignments)
834.496 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFGQTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	85.6	108	2	Q9UL77_HUMAN
2	449.5	82.8	107	2	Q96SA9_homo sapien
3	439.5	80.9	107	2	Q9UL81_HUMAN
4	439	80.8	236	2	Q6GMX0_homo sapien
5	436	80.3	129	1	KV1W_HUMAN
6	436	80.3	236	2	Q6GMX8_homo sapien
7	434	79.9	236	2	Q6GMW1_HUMAN
8	433	79.7	108	1	KV1E_HUMAN
9	430	79.2	108	1	KV1H_HUMAN
10	424	78.1	236	2	Q6PIH7_HUMAN
11	422	77.7	108	2	Q9UL79_HUMAN
12	420	77.3	108	1	KV1N_HUMAN
13	420	77.3	108	2	Q9UL70_HUMAN
14	418	77.0	234	2	Q7Z473_HUMAN
15	416	76.6	108	1	KV1F_HUMAN
16	414	76.2	108	1	KV1K_HUMAN
17	413	76.1	108	1	KV1V_HUMAN
18	412	75.9	108	1	KV1O_HUMAN
19	412	75.9	236	2	Q7Z3Y4_HUMAN
20	411	75.7	236	2	Q502W4_HUMAN
21	409	75.3	108	1	KV1G_HUMAN
22	408	75.1	108	1	KV1M_HUMAN
23	407	75.0	108	1	KV1B_HUMAN
24	406	74.8	108	1	KV1R_HUMAN
25	406	74.8	234	2	Q6FEF6_HUMAN
26	404	74.4	108	1	KV1A_HUMAN
27	404	74.4	189	2	Q569I7_HUMAN
28	400	73.7	236	2	Q6PIH4_HUMAN
29	399.5	73.6	107	1	KVID_HUMAN
30	399	73.5	108	1	KV1S_HUMAN
31	398	73.3	108	1	KV1P_HUMAN

Query Match 85.6%; Score 465; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. NO. 2e-41;

ALIGNMENTS

RESULT 1
Q9UL77_HUMAN
ID Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL [2]
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

32	397	73..1	108	1	KV1L_HUMAN	P01604 homo sapien
33	397	73..1	129	1	KV1X_HUMAN	P04432 homo sapien
34	397	73..1	236	2	Q6GMX9_HUMAN	Q6gmX9 homo sapien
35	396	72.9	108	1	KV1Y_HUMAN	P80362 homo sapien
36	396	72.9	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
37	394	72.6	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
38	391	72.0	108	1	KV1Q_HUMAN	P01609 homo sapien
39	391	72.0	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
40	385.5	71.0	109	1	KV1T_HUMAN	P01612 homo sapien
41	384	70.7	108	1	KV1C_HUMAN	P01595 homo sapien
42	376	69.2	108	1	KV5T_MOUSE	P01653 mus musculu
43	373	68.7	108	1	KV5S_MOUSE	P01652 mus musculu
44	371	68.3	108	2	Q9UL83_HUMAN	Q9ul83 homo sapien
45	371	68.3	116	2	Q96PF6_HUMAN	Q96pf6 homo sapien

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 OS Homo sapiens (Human).
 DE Hypothetical protein.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grunwald J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073775; AAH73775.1; -, mRNA.
 DR SMR; Q6GMX0; 23-236.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

 Query Match 80.8%; Score 439; DB 2; Length 236;
 Best Local Similarity 81.1%; Pred. No. 2.8e-38;
 Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

 QY 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKGKAPKLLIYAASLSQGVPSRF 60
 DB 25 QMTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKGKAPKLLIYAASLSQGVPSRF 84

 QY 61 SGSGYGTDFTLTISSLPQDFPASYQCQESLSASYTFGGTKVEIKR 106
 DB 85 SGSGSGTDFTLTISSLPQDFPASYQCQESLSASYTFGGTKVEIKR 130

 RESULT 5
 KV1W HUMAN STANDARD; PRT; 129 AA.
 ID KV1W HUMAN
 AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DT Ig kappa chain V-I region Walker precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=85014148; PubMed=6091049;
 RA Klobbeck H.G., Combratio G., Zachau H.G.;
 RA "Immunoglobulin genes of the kappa light chain type from two human
 RT lymphoid cell lines are closely related";
 RL Nucleic Acids Res. 12:6995-7006 (1984).
 CC -----
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 CC removed.
 CC -----
 CC EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
 DR PIR; A01883; KIHUWK.
 DR HSP; P01607; 1BWV.
 DR SMR; P04431; 23-129.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR GO; GO:0005576; C: extracellular region; NAS.
 DR GO; GO:0003823; F: antigen binding; NAS.
 DR GO; GO:0006955; P: immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 129 Ig kappa chain V-I region Walker.
 FT REGION 23 45 Framework-1.
 FT REGION 46 56 Complementarity-determining-1.
 FT REGION 57 71 Framework-2.
 FT REGION 72 78 Complementarity-determining-2.
 FT REGION 79 110 Complementarity-determining-3.
 FT REGION 111 119 Complementarity-determining-4.
 FT REGION 120 129 Framework-4.
 FT DISULFID 45 110 By similarity.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

 Query Match 80.3%; Score 436; DB 1; Length 129;
 Best Local Similarity 81.9%; Pred. No. 3e-38;
 Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

 QY 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKGKAPKLLIYAASLSQGVPSRF 60
 DB 25 QMTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKGKAPKLLIYAASLSQGVPSRF 84

 QY 61 SGSGYGTDFTLTISSLPQDFPASYQCQESLSASYTFGGTKVEIK 105
 DB 85 SGSGSGTDFTLTISSLPQDFPASYQCQESLSASYTFGGTKVEIK 129

 RESULT 6
 Q6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.
 ID Q6GMX8 HUMAN
 AC Q6GMX8;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.


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RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -----
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CC removed.
CC -----
CC PIR: A01865; KIHUDE.
DR HSP: P01607; IBW.
DR SNR: P01597; 4-108.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT REGION 99 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;
Best Local Similarity 77.4%; Pred. No. 5.1e-38;
Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCASQRIYNTYVQHPKAPKLLIYAASLSQSGVPSRF 60
Db 3 ZMTQSPSSLSASVGDRTVITCRAGSVNKNYLNWYQKPKAPKVLIFAAASLSKSGVPSRF 62

Qy 61 SSGSGYGTDTLTITSLQPEDFASVYCOESLSASVTFGGTKVEIKR 106
Db 63 SSGSGYGTDTLTITSLQPEDFATYVCOQSYTPTPTFGGTVEMTR 108

RESULT 9
KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-1 region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Geyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A01868; KIHUHU.
DR PDB: 1F6L; X-ray; L=1-108.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT REGION 99 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.2%; Score 430; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 1.1e-37;
Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCASQRIYNTYVQHPKAPKLLIYAASLSQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSYLSWYQKPKAPKVLIFAAASLSKSGVPSRF 62

Qy 61 SSGSGYGTDTLTITSLQPEDFASVYCOESLSASVTFGGTKVEIKR 106
Db 63 SSGSGYGTDTLTITSLQPEDFATYVCOQNYTPTPTFGGTVEMTR 108

RESULT 10
Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
ON NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."; [2]
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RC NIH MGC Project;
RG Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034141; AAH34141.1; -, mRNA.
DR HSP; P01607; IAR2.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 78.1%; Score 424; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 1.le-36;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVCDRVITISCRASORINTYLNWYQHKGKAPKLLIYAASLSQSGVPSRF 60
DB 25 QLTQSPFLSASVCDRVITISCRASQGISYSLAWYQQKPKAPPELLIYAASLTQSGVPSRF 84

QY 61 SGSGYGTDFLTITISSLOFEDFASVYCOESLSASVTFQGGTKVEIKR 106
DB 85 SGSGGTDFLTITISSLOFEDFATVYCOQLNSPPTFGGTKVEIKR 130

RESULT 11
Q9UL79 HUMAN
ID Q9UL79 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277133; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."; [2]
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=1601042;
RX Huber C., Klobbeck H.G., Zachau H.G.;
RA "Ongoing V kappa-J kappa recombination after formation of a productive
RT V kappa-J kappa coding joint."; [3]
RL Eur. J. Immunol. 22:1561-1565(1992).
RN NUCLEOTIDE SEQUENCE.
RP PubMed=8436174;
RX Wagner S.D., Luzzatto L.;

RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."; [2]
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035035; AAD56271.1; -, mRNA.
DR PIR; S23638; S23638.
DR PIR; S30521; S30521.
DR PIR; S34090; S34090.
DR HSP; P01607; 1BW.
DR SMR; Q9UL79; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1_1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 77.7%; Score 422; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 7.5e-37;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSLASVCDRVITISCRASORINTYLNWYQHKGKAPKLLIYAASLSQSGVPSRF 61
DB 4 MTQSPSLASVCDRVITISCRMSQGISYSLAWYQQKPKAPPELLIYAASLTQSGVPSRF 63

QY 62 GSGYGTDFLTITISSLOFEDFASVYCOESLSASVTFQGGTKVEIKR 106
DB 64 GSGGTDFLTITISSLOFEDFATVYCOQYSPPTFGGTKVEIKR 108

RESULT 12
KVIN HUMAN
ID KVIN HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."; [2]
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
[3]
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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[4]
DR PIR; A01872; K1HUOU.
DR HSP; P01607; 1BW.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.

FT REGION 24 34 Complementarity-determining-1.
 FT REGION 35 49 Framework-2.
 FT REGION 50 56 Complementarity-determining-2.
 FT REGION 57 88 Framework-3.
 FT REGION 89 97 Complementarity-determining-3.
 FT REGION 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11779 MW; 8283D4A24105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
 Best Local Similarity 68.9%; Pred. No. 1.2e-36;
 Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
 DB 3 QMTZSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 62

QY 61 SSGSGYGTDTLTITSSLOPDPFASYYCOESLSASYTFGQTKVEIKR 106
 DB 63 SSGSGGTDTLTITSSLOPDPVATYYCOKYNAPRTFGPGTKLEIKR 108

RESULT 13
 Q9UL70 HUMAN
 ID Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
 AC Q9UL70; 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment)
 DE DE
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=1660528;
 RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghosssein C., Smith A., Diamond B.; characteristics of antibodies bearing an anti-DNA-associated idiotype.";
 RT J. Exp. Med. 174:1639-1652 (1991).
 RL EMBL; AF035044; AAD56280.1; -; mRNA.
 DR PIR; P08663; PH0863.
 DR HSP; P01607; 1BW.
 DR SMR; Q9UL70; 1-108.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 77.3%; Score 420; DB 2; Length 108;
 Best Local Similarity 79.2%; Pred. No. 1.2e-36;
 Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60
 DB 3 QMTZSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 62

QY 61 SSGSGYGTDTLTITSSLOPDPFASYYCOESLSASYTFGQTKVEIKR 106
 DB 63 SSGSGGTDTLTITSSLOPDPVATYYCOKYNAPRTFGPGTKLEIKR 108

RESULT 14
 Q72473 HUMAN
 ID Q72473 HUMAN PRELIMINARY; PRT; 234 AA.
 AC Q72473; 2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGKC protein.
 GN Name=IGKC;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fhery J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 NIH MGC Project;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC056256; AAS56256.1; -; mRNA.
 DR HSP; P01834; 1HEZ.
 DR SMR; Q72473; 22-234.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.0%; Score 418; DB 2; Length 234;
 Best Local Similarity 77.1%; Pred. No. 4.8e-36;
 Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGRVITISCRASQRIINTYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
 DB 24 MTQSPSSASVGRVITISCRASQSIQSLAWYQKPGKAPQLLIYAASTLQSGVPSRF 83

QY 62 SSGYGTDTLTITSSLOPDPFASYYCOESLSASYTFGQTKVEIKR 106
 DB 63 SSGYGTDTLTITSSLOPDPVATYYCOKYNAPRTFGPGTKLEIKR 108

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:36:55 ; Search time 22.6455 Seconds
(without alignments)

386.993 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFGQTKVEIKR 106

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475	87.5	107	1	US-08-276-852-104
2	475	87.5	107	1	US-08-899-575-104
3	475	87.5	107	1	US-08-899-575-104
4	475	87.5	107	4	PCT-US95-08743-104
5	474	87.3	107	2	US-09-240-274-179
6	474	87.3	107	2	US-09-848-798-179
7	472	86.9	107	2	US-09-240-274-33
8	472	86.9	107	2	US-09-240-274-175
9	472	86.9	107	2	US-09-240-274-176
10	472	86.9	107	2	US-09-848-798-33
11	472	86.9	107	2	US-09-848-798-175
12	472	86.9	107	2	US-09-848-798-176
13	471	86.7	107	2	US-09-240-274-156
14	471	86.7	107	2	US-09-848-798-156
15	468	86.2	107	2	US-09-240-274-36
16	468	86.2	107	2	US-09-848-798-36
17	467	86.0	107	1	US-08-276-852-105
18	467	86.0	107	1	US-08-899-575-105
19	467	86.0	107	4	PCT-US95-08743-105
20	467	85.0	107	2	US-09-240-274-32
21	464.5	85.5	108	2	US-09-240-274-43
22	464.5	85.5	108	2	US-09-848-798-32
23	464.5	85.5	108	2	US-09-848-798-43
24	464.5	85.5	108	2	US-09-240-274-37
25	464	85.5	107	2	US-09-848-798-37
26	464	85.5	107	2	US-09-192-854-2
27	464	85.5	240	2	US-09-192-854-2

Sequence 2, Appli
Sequence 38, Appl
Sequence 39, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 158, App
Sequence 158, App
Sequence 167, App
Sequence 167, App
Sequence 163, App
Sequence 163, App
Sequence 35, Appl
Sequence 173, App
Sequence 35, Appl
Sequence 173, App
Sequence 173, App
Sequence 29, Appl
Sequence 106, App
Sequence 106, App

28 464 85.5 240 2 US-09-511-939-2
29 462 85.1 107 2 US-09-240-274-38
30 462 85.1 107 2 US-09-240-274-39
31 462 85.1 107 2 US-09-848-798-38
32 462 85.1 107 2 US-09-848-798-39
33 461 84.9 107 2 US-09-240-274-158
34 461 84.9 107 2 US-09-848-798-158
35 460.5 84.8 108 2 US-09-240-274-167
36 460.5 84.8 108 2 US-09-848-798-167
37 459.5 84.6 108 2 US-09-240-274-163
38 459.5 84.6 108 2 US-09-848-798-163
39 458 84.3 107 2 US-09-240-274-35
40 458 84.3 107 2 US-09-240-274-173
41 458 84.3 107 2 US-09-848-798-35
42 458 84.3 107 2 US-09-848-798-173
43 458 84.3 108 1 US-08-379-057-29
44 457 84.2 104 1 US-08-276-852-106
45 457 84.2 104 1 US-08-899-575-106

ALIGNMENTS

RESULT 1
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; TYPE: 107 amino acids
; LENGTH: 107 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-104

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Query Match      87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
   |||||
Db 1 ELTQSPSSLASVGDRTVITISCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
   |||||

QY 61 SGSGYGTDFLTITSSLOFEDFASYQCESLSASVTFQGGTKVEIKR 106
   |||||
Db 61 SGSGGTDFLTITSSLOPEDFATYYCQOSYSTPTTQGGTKLEIKR 106
   |||||

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
   |||||
Db 1 ELTQSPSSLASVGDRTVITISCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
   |||||

QY 61 SGSGYGTDFLTITSSLOFEDFASYQCESLSASVTFQGGTKVEIKR 106
   |||||
Db 61 SGSGGTDFLTITSSLOPEDFATYYCQOSYSTPTTQGGTKLEIKR 106
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RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
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QY 61 SGSGYGTDFLTITSSLOFEDFASYQCESLSASVTFQGGTKVEIKR 106
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Db 61 SGSGGTDFLTITSSLOPEDFATYYCQOSYSTPTTQGGTKLEIKR 106
   |||||

RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match      87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
   |||||
Db 1 ELTQSPSSLASVGDRTVITISCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
   |||||

QY 61 SGSGYGTDFLTITSSLOFEDFASYQCESLSASVTFQGGTKVEIKR 106
   |||||
Db 61 SGSGGTDFLTITSSLOPEDFATYYCQOSYSTPTTQGGTKLEIKR 106
   |||||

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
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GENERAL INFORMATION:
APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)
CURRENT APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PCT APPLICATION DATA:
PCT APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-104

Query Match 87.5%; Score 475; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 60

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGTKVEIKR 106
DB 61 SGSGYGTDFLTITSSLOPEDFATYTCQSYSTPTTFGGTKLEIKR 106

RESULT 5

US-09-240-274-179
Sequence 179, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match 87.3%; Score 474; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSMSASVGDRTVITCRASQSIGTYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGTKVEIKR 106
DB 62 SGSGYGTDFLTITSSLOPEDFATYTCQSYSTPTTFGGTKVEIKR 107

RESULT 6

US-09-848-798-179
Sequence 179, Application US/09848798
Patent No. 6858719
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PCT APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match 87.3%; Score 474; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSMSASVGDRTVITCRASQSIGTYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGTKVEIKR 106
DB 62 SGSGYGTDFLTITSSLOPEDFATYTCQSYSTPTTFGGTKVEIKR 107

RESULT 7

US-09-240-274-33
Sequence 33, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.6e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQSISSYLNWYQHPGKAPKLLIYAASSLSQSGVPSRF 61

Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SGSGYGTDFLTITISSLOFEDFASYCQESLSASVTFQGGTKVEIKR 106
Db 62 SGSGGTDFLTITISSLOPEDFATYCCQSYSTPTWTFQGGTKVEIKR 107

RESULT 12

US-09-848-798-176
; Sequence 176, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 86.9%; Score 472; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.6e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SGSGYGTDFLTITISSLOFEDFASYCQESLSASVTFQGGTKVEIKR 106
Db 62 SGSGGTDFLTITISSLOPEDFATYCCQSYSTPTWTFQGGTKVEIKR 107

RESULT 13

US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match 86.7%; Score 471; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 3.2e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SGSGYGTDFLTITISSLOFEDFASYCQESLSASVTFQGGTKVEIKR 106
Db 62 SGSGGTDFLTITISSLOPEDFATYCCQSYSTPTWTFQGGTKLEIKR 107

RESULT 14

US-09-848-798-156
; Sequence 156, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match 86.7%; Score 471; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 3.2e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SGSGYGTDFLTITISSLOFEDFASYCQESLSASVTFQGGTKVEIKR 106
Db 62 SGSGGTDFLTITISSLOPEDFATYCCQSYSTPTWTFQGGTKLEIKR 107

RESULT 15

US-09-240-274-36
; Sequence 36, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-36

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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-36

Query Match      86.2%; Score 468; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 6.2e-38;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITCRASQSIIRRYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 61

Qy 61 SSGSGYGTDFLTITSSLPQFDPASYCOESLSASVTFGGQTKVEIKR 106
Db 62 TSGSGYGTDFLTITSSLPQFDPASYCOESLSASVTFGGQTKVEIKR 107
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Search completed: April 3, 2006, 14:40:34
Job time : 22.6455 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 15:10:27 ; Search time 72.4333 Seconds
(without alignments)
611.458 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	106	4	US-10-027-725A-10
2	475	87.5	107	4	US-10-016-986-104
3	474	87.3	107	3	US-09-848-798-179
4	472	86.9	107	3	US-09-848-798-33
5	472	86.9	107	3	US-09-848-798-175
6	472	86.9	107	3	US-09-848-798-176
7	471	86.7	107	3	US-09-848-798-156
8	468	86.2	107	3	US-09-848-798-36
9	468	86.2	116	5	US-10-783-311-198
10	467	86.0	107	4	US-10-016-986-105
11	465	85.6	111	4	US-10-203-754A-57
12	464.5	85.5	108	3	US-09-848-798-32
13	464.5	85.5	108	3	US-09-848-798-43
14	464	85.5	107	3	US-09-848-798-37
15	464	85.5	108	4	US-10-409-814A-4
16	464	85.5	240	3	US-09-192-854-2
17	464	85.5	240	3	US-09-968-561A-2
18	464	85.5	240	3	US-09-968-744A-2
19	464	85.5	240	3	US-09-968-561A-2
20	464	85.5	240	5	US-10-744-774-1
21	464	85.5	240	6	US-11-115-682-2
22	463	85.3	107	3	US-09-791-153A-67
23	463	85.3	108	5	US-10-726-332-214
24	463	85.3	108	5	US-10-805-177-64
25	462	85.1	106	4	US-10-027-725A-12
26	462	85.1	107	3	US-09-848-798-38
27	462	85.1	107	3	US-09-848-798-39

28	462	85.1	108	5	US-10-744-774-15	Sequence 15, Appl
29	462	85.1	108	5	US-10-805-177-20	Sequence 20, Appl
30	461	84.9	107	3	US-09-848-798-158	Sequence 158, App
31	461	84.9	108	5	US-10-726-332-18	Sequence 18, Appl
32	460.5	84.8	108	3	US-09-848-798-167	Sequence 167, App
33	460	84.7	106	4	US-10-027-725A-11	Sequence 11, Appl
34	460	84.7	106	4	US-10-466-242-38	Sequence 38, Appl
35	460	84.7	106	4	US-10-466-242-56	Sequence 56, Appl
36	460	84.7	108	5	US-10-726-332-28	Sequence 27, Appl
37	460	84.7	157	6	US-11-131-648-27	Sequence 63, Appl
38	460	84.7	157	6	US-11-131-648-63	Sequence 163, App
39	459.5	84.6	108	3	US-09-848-798-163	Sequence 209, App
40	459	84.5	108	5	US-10-726-332-209	Sequence 100, App
41	459	84.5	111	5	US-10-916-840-100	Sequence 35, Appl
42	458	84.3	107	3	US-09-848-798-35	Sequence 173, App
43	458	84.3	107	3	US-09-848-798-173	Sequence 90, Appl
44	458	84.3	108	5	US-10-477-830-90	Sequence 55, Appl
45	458	84.3	111	4	US-10-203-754A-56	

ALIGNMENTS

RESULT 1
US-10-027-725A-10
; Sequence 10, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgG-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-10

Query Match 100.0%; Score 543; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.7e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ELTQSPSSLSASVGDRTVISCRASQRTINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF	60
Db	1	ELTQSPSSLSASVGDRTVISCRASQRTINTYLNWQHKGKAPKLLIYAASSLSQGVPSRF	60
Qy	61	SGSGYGTDTLTITISLQFEDFASVYCOESLSASYTFGGTKVEIKR	106
Db	61	SGSGYGTDTLTITISLQFEDFASVYCOESLSASYTFGGTKVEIKR	106

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016.986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24

```
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      87.5%; Score 475; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 6.2e-36;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGTDFLTITSSLOFEDFASYYCOESLSASVTFQGTKEIKR 106
Db 61 SSGSGTDFLTITSSLOFEDFATYYCQSYSTPTFTFGQTKLEIKR 106

RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match      87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 7.7e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSMSASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFLTITSSLOFEDFASYYCOESLSASVTFQGTKEIKR 106
Db 62 SSGSGTDFLTITSSLOFEDFATYYCQSYSTPTFTFGQTKVEIKR 107

RESULT 4
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-848-798-33

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.2e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFLTITSSLOFEDFASYYCOESLSASVTFQGTKEIKR 106
Db 62 SSGSGTDFLTITSSLOFEDFATYYCQSYSTPTFTFGQTKVEIKR 107

RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.2e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLASVGDRTVITICRASQRTINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFLTITSSLOFEDFASYYCOESLSASVTFQGTKEIKR 106
Db 62 SSGSGTDFLTITSSLOFEDFATYYCQSYSTPTFTFGQTKVEIKR 107

RESULT 6
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US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
; US-09-848-798-176

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.2e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIYLNWYOHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61

Qy 61 SSGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGQTKVEIKR 106
Db 62 SSGSGYGTDFLTITSSLOPEDFATYCCQSYSTPTFTFGGQTKVEIKR 107

RESULT 7
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
; US-09-848-798-156

Query Match      86.7%; Score 471; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.4e-35;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIYLNWYOHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSRSGVPSRF 61

Qy 61 SSGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGQTKVEIKR 106
Db 62 SSGSGYGTDFLTITSSLOPEDFATYCCQSYSTPTFTFGGQTKLEIKR 107

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RESULT 8
US-09-848-798-36
; Sequence 36, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 105
; US-09-848-798-36

Query Match      86.2%; Score 468; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.7e-35;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIYLNWYOHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61

Qy 61 SSGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGQTKVEIKR 106
Db 62 TSGSGYGTDFLTITSSLOPEDFATYCCQSYSTPTFTFGGQTKVEIKR 107

RESULT 9
US-10-783-311-198
; Sequence 198, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
; US-10-783-311-198

Query Match      86.2%; Score 468; DB 5; Length 116;
Best Local Similarity 85.8%; Pred. No. 3e-35;
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIYLNWYOHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 4 QMTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 63

Qy 61 SSGSGYGTDFLTITSSLOPEDFASYCQESLSASVTFGGQTKVEIKR 106

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      85.5%; Score 464.5; DB 3; Length 108;
Best Local Similarity 86.9%; Pred. No. 5.7e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SSGSGYGTDFTLTISLQPEDFASYCQESLSA-SYTFGQGTKEIKR 106
Db 62 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPTPTFGQGTKEIKR 108

RESULT 14
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      85.5%; Score 464; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 6.3e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 61
QY 61 SSGSGYGTDFTLTISLQPEDFASYCQESLSASVTFGQGTKEIKR 106
Db 62 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPTPTFGQGTKEIKR 107

RESULT 15
US-10-409-814A-4
; Sequence 4, Application US/10409814A
; Publication No. US20040202995A1
; GENERAL INFORMATION:
; APPLICANT: de Wildt, Rudolf
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND SCREENING METHODS
; FILE REFERENCE: 8039/2032
; CURRENT APPLICATION NUMBER: US/10/409,814A
; CURRENT FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-409-814A-4

Query Match      85.5%; Score 464; DB 4; Length 108;
Best Local Similarity 85.8%; Pred. No. 6.4e-35;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
Db 3 OMTQSPSSLSASVGDRTVITSCRASQSISSYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 62
QY 61 SSGSGYGTDFTLTISLQPEDFASYCQESLSASVTFGQGTKEIKR 106
Db 63 SSGSGGTDFTLTISLQPEDFATYCCQSYSTPTPTFGQGTKEIKR 108

Search completed: April 3, 2006, 15:20:24
Job time : 72.4333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:13:12 ; Search time 9.63636 Seconds
(without alignments)
334.861 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASYTFGQTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
8: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474	87.3	107	7	US-11-064-174-179
2	472	86.9	107	7	US-11-064-174-33
3	472	86.9	107	7	US-11-064-174-175
4	472	86.9	107	7	US-11-064-174-176
5	471	86.7	107	7	US-11-064-174-156
6	468	86.2	107	7	US-11-064-174-36
7	464.5	85.5	108	7	US-11-064-174-32
8	464.5	85.5	108	7	US-11-064-174-43
9	464	85.5	107	7	US-11-064-174-37
10	464	85.5	108	6	US-10-925-366A-3
11	464	85.5	108	6	US-10-925-366A-6
12	464	85.5	108	7	US-11-102-512-3
13	464	85.5	108	7	US-11-102-512-6
14	464	85.5	240	6	US-10-925-366A-219
15	462	85.1	107	7	US-11-064-174-38
16	462	85.1	107	7	US-11-064-174-39
17	462	85.1	109	7	US-11-127-932-17
18	462	85.1	109	7	US-11-127-932-16
19	462	85.1	109	7	US-11-127-932-20
20	462	85.1	109	7	US-11-127-903-17
21	462	85.1	109	7	US-11-127-903-16
22	462	85.1	109	7	US-11-127-903-20
23	461	84.9	107	7	US-11-064-174-158
24	461	84.9	108	6	US-10-771-257-36
25	461	84.9	108	7	US-11-127-677-36

26	460.5	84.8	108	7	US-11-064-174-167	Sequence 167, App
27	459.5	84.6	108	7	US-11-064-174-163	Sequence 163, App
28	459	84.5	111	7	US-11-049-536-100	Sequence 100, App
29	458	84.5	111	7	US-11-199-739-100	Sequence 100, App
30	458	84.3	107	7	US-11-064-174-35	Sequence 35, App
31	458	84.3	107	7	US-11-064-174-173	Sequence 173, App
32	457	84.2	107	7	US-11-064-174-40	Sequence 40, App
33	457	84.2	214	7	US-11-128-900-71	Sequence 71, App
34	456	84.0	107	7	US-11-064-174-44	Sequence 44, App
35	456	84.0	108	6	US-10-771-257-28	Sequence 28, App
36	456	84.0	108	7	US-11-127-677-28	Sequence 28, App
37	456	84.0	236	7	US-11-086-289-8	Sequence 8, App
38	453	83.4	105	7	US-11-155-775-52	Sequence 52, App
39	452	83.2	107	7	US-11-064-174-172	Sequence 172, App
40	452	83.2	107	7	US-11-064-174-174	Sequence 174, App
41	452	83.2	108	7	US-11-049-536-452	Sequence 452, App
42	452	83.2	108	7	US-11-199-739-452	Sequence 452, App
43	451.5	83.1	108	7	US-11-064-174-41	Sequence 41, App
44	451	83.1	107	7	US-11-064-174-168	Sequence 168, App
45	451	83.1	108	6	US-10-834-397-14	Sequence 14, App

ALIGNMENTS

RESULT 1
US-11-064-174-179
; Sequence 179, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION: Donald L.
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-064-174-179

Query Match	87.3%	Score	474	DB	7	Length	107
Best Local Similarity	87.7%	Pred. No.	3.5e-33				
Matches	93	Conservative	5	Mismatches	8	Indels	0
						Gaps	0
Qy	1	ELTQSPSSLSASVGDRTVISCRASQRIINTYLNWYQHKFGKAPKLLIYAASLSQGVPSRF	60				
Db	2	ELTQSPSSMSASVGDRTVITCEASQSIGTYLNWYQKFGKAPKLLIYAASLSQGVPSRF	61				
Qy	61	SGSGYGTDTLTITSSLOPEDFASYCQESLSASTFGQTKVEIKR	106				
Db	62	SGSGYGTDTLTITSSLOPEDFATYCCQSYSTPTWTFGQTKVEIKR	107				

RESULT 2
US-11-064-174-33
; Sequence 33, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

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; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-11-064-174-33

Query Match      86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.1e-33;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITICRASQRIYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
    |||||
Db 2 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
    |||||

QY 61 SSGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTKEIKR 106
    |||||
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTLWTFQGTKEIKR 107
    |||||

RESULT 3
US-11-064-174-175
; Sequence 175, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-064-174-175

Query Match      86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.1e-33;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITICRASQRIYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
    |||||
Db 2 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
    |||||

QY 61 SSGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTKEIKR 106
    |||||
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTLWTFQGTKEIKR 107
    |||||

RESULT 4
US-11-064-174-176
; Sequence 176, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-064-174-176

Query Match      86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.1e-33;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITICRASQRIYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
    |||||
Db 2 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
    |||||

QY 61 SSGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTKEIKR 106
    |||||
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTLWTFQGTKEIKR 107
    |||||
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US-11-064-174-176
; Sequence 176, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-064-174-176

Query Match      86.9%; Score 472; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 5.1e-33;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITICRASQRIYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
    |||||
Db 2 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
    |||||

QY 61 SSGSGYGTDFLTITSSLOFEDFASYCOESLSASVTFQGTKEIKR 106
    |||||
Db 62 SSGSGGTDFLTITSSLOPEDFATYCCQSYSTLWTFQGTKEIKR 107
    |||||

RESULT 5
US-11-064-174-156
; Sequence 156, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-064-174-156

Query Match      86.7%; Score 471; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 6.2e-33;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITICRASQRIYLNWYQHKPGKAPKLLIYAASSLSQSGVPSRF 60
    |||||
Db 2 ELTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61
    |||||
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```
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-11-064-174-37

Query Match      85.5%; Score 464; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.4e-32; Indels 0; Gaps 0;
Matches 91; Conservative 7; Mismatches 8;

QY 1 ELTQSPSSLSASVGDRTVITICRASQRIYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITICRASQSISSVLYNQYQKPGKAPKLLIYAASSLSQGVPSRF 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFTLTISLQFEDFASYCQESLSASVYTFGGTKVIEKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGSGSGTDFTLTISLQPEDFATYYCQSYSTPTTFGGTKVIEKR 107
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-925-366A-3
; Sequence 3, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demidov, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Baaran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Artificial Antibody Domain Sequence
US-10-925-366A-3

Query Match      85.5%; Score 464; DB 6; Length 108;
Best Local Similarity 85.8%; Pred. No. 2.4e-32; Indels 0; Gaps 0;
Matches 91; Conservative 7; Mismatches 8;

QY 1 ELTQSPSSLSASVGDRTVITICRASQRIYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGDRTVITICRASQSISSVLYNQYQKPGKAPKLLIYAASSLSQGVPSRF 62
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGSGYGTDFTLTISLQFEDFASYCQESLSASVYTFGGTKVIEKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFTLTISLQPEDFATYYCQSYSTPTTFGGTKVIEKR 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-11-102-512-3
; Sequence 3, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/2132B
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
```

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; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-512-3

Query Match      85.5%; Score 464; DB 7; Length 108;
Best Local Similarity 85.8%; Pred. No. 2.4e-32;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SGSGYGTDFLTITISLQFEDFASYCOESLSASVTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGGTDFLTITISLQPEDFATYCCQSYSTPTNFTFGGTVKVEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-11-102-512-6
; Sequence 6, Application US/11102512
; Publication No. US20060062784A1
; GENERAL INFORMATION:
; APPLICANT: Grant et al., S.
; TITLE OF INVENTION: Compositions monovalent for CD40L binding and methods of use
; FILE REFERENCE: 8039/21328
; CURRENT APPLICATION NUMBER: US/11/102,512
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/610,819
; PRIOR FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primary amino acid sequence of Vk dummy
US-11-102-512-6

Query Match      85.5%; Score 464; DB 7; Length 108;
Best Local Similarity 85.8%; Pred. No. 2.4e-32;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SGSGYGTDFLTITISLQFEDFASYCOESLSASVTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGGTDFLTITISLQPEDFATYCCQSYSTPTNFTFGGTVKVEIKR 108
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RESULT 14
US-10-925-366A-219
; Sequence 219, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Dewildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
```

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; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 219
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Antibody Sequence, VH and VL joined by Gly4Ser Linker
US-10-925-366A-219

Query Match      85.5%; Score 464; DB 6; Length 240;
Best Local Similarity 85.8%; Pred. No. 4.8e-32;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLASVGDRTVITICRASQRIINTYLNWYQHKPGKAPKLLIYAASSLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 QMTQSPSSLASVGDRTVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 194
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SGSGYGTDFLTITISLQFEDFASYCOESLSASVTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 SGSGGTDFLTITISLQPEDFATYCCQSYSTPTNFTFGGTVKVEIKR 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-11-064-174-38
; Sequence 38, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-11-064-174-38

Query Match      85.1%; Score 462; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 3.5e-32;
```

Matches	92;	Conservative	5;	Mismatches	9;	Indels	0;	Gaps	0;
Qy	1	ELTQSPSSLASVGDRTVITISCRASQRIINTYLNWYOHKPGKAPKLLIYAASSLQSGVPSRF	60						
Db	2	ELTQSPSSLASVGDRTVITISCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF	61						
Qy	61	SGSGYGTDFTLTITSSLOQDFASYYQESLSASVTFGGTKVEIKR	106						
Db	62	SGSGYGTDFTLTITSSLOQDFATYYCOQSYSTPRTFGGTKVEIKR	107						

Search completed: April 3, 2006, 15:21:30
Job time : 9.63636 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:09 ; Search time 92.1879 Seconds
(without alignments)
505.209 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSFSSLSASVGDRTTIT.....QQSYTTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Geneseq 21:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2000s:*
5: geneseqp2000s:*
6: geneseqp2000s:*
7: geneseqp2000s:*
8: geneseqp2000s:*
9: geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537	98.2	106	5	ABG30449 Human IgE
2	484	88.5	107	2	AAR54260 Anti-HIV
3	484	88.5	107	2	AAW01283 VL region
4	484	88.5	107	3	AAY98244 Anti-gp12
5	484	88.5	107	3	AAY95135 Anti-gp12
6	483	88.3	107	4	AAG93590 Human ant
7	483	88.3	107	6	ABO27397 Anti-Rh(D
8	480	87.8	107	4	AAG93644 Human ant
9	480	87.8	107	6	ABO27451 Anti-Rh(D
10	476	87.0	107	2	AAR54261 Anti-HIV
11	476	87.0	107	2	AAW01284 VL region
12	476	87.0	107	3	AAY98245 Anti-gp12
13	476	87.0	107	3	AAY95136 Anti-gp12
14	475	86.8	107	4	AAG93663 Human ant
15	475	86.8	107	4	AAG93664 Human ant
16	475	86.8	107	6	ABO27471 Anti-Rh(D
17	475	86.8	107	6	ABO27470 Anti-Rh(D
18	474	86.7	107	4	AAG93667 Human ant
19	474	86.7	107	6	ABO27474 Anti-Rh(D
20	473.5	86.6	108	4	AAG93589 Human ant
21	473.5	86.6	108	4	AAG93600 Human ant
22	473.5	86.6	108	6	ABO27407 Anti-Rh(D
23	473.5	86.6	108	6	ABO27396 Anti-Rh(D
24	473	86.5	107	4	AAG93594 Human ant

25	473	86.5	107	6	ABO27401 Anti-Rh(D
26	473	86.5	109	8	ADP66620 Anti-RAS
27	473	86.5	109	8	ADP66619 Anti-RAS
28	473	86.5	109	8	ADP66623 Anti-RAS
29	473	86.5	109	8	ADP66623 Anti-RAS
30	473	86.5	109	8	ADP66623 Anti-RAS
31	473	86.5	109	8	ADP66623 Anti-RAS
32	473	86.5	111	4	AAG63656 Amino aci
33	473	86.5	111	6	ABJ38615 Hepatitis
34	473	86.5	240	6	ABJ38595 Hepatitis
35	473	86.5	244	8	ADP75290 Immunoglo
36	473	86.5	299	4	AAG63660 Amino aci
37	472.5	86.4	108	4	AAG93655 Human ant
38	472.5	86.4	108	6	ABO27462 Anti-Rh(D
39	472	86.3	107	4	AAG93596 Human ant
40	472	86.3	107	4	AAG93650 Human ant
41	472	86.3	107	4	AAG93595 Human ant
42	472	86.3	107	6	ABO27457 Anti-Rh(D
43	472	86.3	107	6	ABO27403 Anti-Rh(D
44	472	86.3	107	6	ABO27402 Anti-Rh(D
45	472	86.3	116	9	ADW04873 PAPP-A im

ALIGNMENTS

RESULT 1
ABG30449
ID ABG30449 standard; protein; 106 AA.
XX AC
XX ABG30449;
DT 21-OCT-2002 (first entry)
XX Human IgE Fab clone 60 light chain protein.
DE Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
KW Homo sapiens.
XX Key
XX Key Location/Qualifiers
FT Region 1..21
FT Region /note= "PR1 region"
FT Region 22..32
FT Region /note= "CDR1 region"
FT Region 33..47
FT Region /note= "PR2 region"
FT Region 48..54
FT Region /note= "CDR2 protein"
FT Region 55..86
FT Region /note= "PR3 region"
FT Region 87..95
FT Region /note= "CDR2 region"
FT Region 96..104
FT Region /note= "PR4 region"
FT Misc-difference 98
FT /note= "Encoded by COT"
XX WO200253595-A1.
XX 11-JUL-2002.
XX 27-DEC-2001; 2001WO-SE002908.
XX 29-DEC-2000; 2000SE-00004892.
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX N-PSDB; ABK89641.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 40; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine againsts a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergenic patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC fab, clone 60 light chain protein of the invention
XX
XX Sequence 106 AA;

Query Match 98.2%; Score 537; DB 5; Length 106;
Best Local Similarity 99.1%; Pred. No. 6.6e-30;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLQPEDFASYCQSYTTLTYTFGSGTKLEIKR 106
DB 61 SGSGSGTEFTLTISNLQPEDFASYCQSYTTLTYTFGSGTKLEIKR 106

RESULT 2
AAR54260
ID AAR54260 standard; protein; 107 AA.

XX AC AAR54260;
XX
XX 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin light chain variable region b22.
XX
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..21 /label= FR1
FT Region	22..33 /label= FR1
FT Region	34..48 /label= FR2
FT Region	49..55 /label= CDR2
FT Region	56..87 /label= FR3
FT Region	88..95 /label= CDR3
FT Region	96..107 /label= FR4

PN WO9407922-A1.

XX 14-APR-1994.
PD
XX 30-SEP-1993; 93WO-US009328.
PF
XX 30-SEP-1992; 92US-00954148.
PR
XX (SCRI) SCRIPPS RES INST.
PA
XX Burton DR, Barbas CF, Lerner RA;
FI
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
PT
XX Claim 5; Page 189; 248pp; English.
PS
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAB regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54260
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 107 AA;

Query Match 88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No. 3e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLQPEDFASYCQSYTTLTYTFGSGTKLEIKR 106
DB 61 SGSGSGTEFTLTISNLQPEDFASYCQSYTTLTYTFGSGTKLEIKR 106

RESULT 3
AAW01283
ID AAW01283 standard; protein; 107 AA.

XX AC AAW01283;
XX
XX 29-JAN-1997 (first entry)
DT
XX VL region of HIV neutralising MAb, clone b22 and B35.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
XX Homo sapiens.

Key	Location/Qualifiers
FT Region	1..21 /label= FR1
FT Region	22..32 /label= CDR1
FT Region	33..47 /label= FR2
FT Region	48..54 /label= CDR2
FT Region	55..86 /label= FR3
FT Region	87..95 /label= CDR3

FT Region 96..107
 PT /label= FR4
 XX
 PN WO9602273-A1.
 XX
 PD 01-FEB-1996.
 XX
 PF 11-JUL-1995; 95WO-US008743.
 XX
 PR 18-JUL-1994; 94US-00276852.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 1996-179601/18.
 XX
 XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
 PT immuno:therapy and detection of HIV infection.
 PT
 XX Example; Fig 11; 366pp; English.
 XX
 XX The sequences given in AA001261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAB's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2 gene
 CC clones, b22 and B35. A MAB containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by
 CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds
 CC mature gp120 preferentially over the precursor gp160. The MAB may be used
 CC for determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection
 XX
 XX SQ Sequence 107 AA;
 Query Match 88.5%; Score 484; DB 2; Length 107;
 Best Local Similarity 88.7%; Pred. No. 3e-26;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ELTQSPSSLSASVGDRTVITTCRARSQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 1 ELTQSPSSLSASVGDRTVITTCRARSQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Qy 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYSTLTFTFGSGTKLEIKR 106
 Db 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYSTLTFTFGSGTKLEIKR 106
 RESULT 4
 AA99244
 ID AA99244 standard; protein; 107 AA.
 XX
 XX AA99244;
 XX
 XX 04-JUL-2000 (first entry)
 XX
 XX Anti-gp120 antibody light chain variable region from clone b22.
 XX
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 XX Homo sapiens.
 XX
 XX AU9948754-A.
 XX
 XX 17-FEB-2000.
 XX
 XX 16-SEP-1999; 99AU-00048754.
 XX
 XX 16-SEP-1999; 99AU-00048754.
 XX

PA (SCRI) SCRIPPS RES INST.
 XX
 XX Burton DR, Barbas CF, Lerner RA;
 XX
 XX WPI; 2000-246867/22.
 XX
 XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX
 XX Example 9; Fig 11; 374pp; English.
 XX
 XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AA99206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 XX
 XX SQ Sequence 107 AA;
 Query Match 88.5%; Score 484; DB 3; Length 107;
 Best Local Similarity 88.7%; Pred. No. 3e-26;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ELTQSPSSLSASVGDRTVITTCRARSQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 1 ELTQSPSSLSASVGDRTVITTCRARSQISSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Qy 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYSTLTFTFGSGTKLEIKR 106
 Db 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYSTLTFTFGSGTKLEIKR 106
 RESULT 5
 AA95135
 ID AA95135 standard; protein; 107 AA.
 XX
 XX AA95135;
 XX
 XX 30-JUN-2000 (first entry)
 XX
 XX Anti-gp120 antibody light chain variable region from clone b22.
 XX
 XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX

OS Homo sapiens.
XX AU9948756-A.
PN 17-FEB-2000.
XX 16-SEP-1999; 99AU-00048756.
XX 16-SEP-1999; 99AU-00048756.
XX (SCRI) SCRIPPS RES INST.
XX Burton DR, Barbas CF, Lerner RA;
XX WPI; 2000-293393/26.
XX Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
XX Example 9; Fig 11; 366pp; English.
XX The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
XX Sequence 107 AA;
SQ
Query Match 88.5%; Score 484; DB 3; Length 107;
Best Local Similarity 88.7%; Pred. No. 3e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTTTCARQSIYLYNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTTTCARQSIYLYNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTYLLTYFGSGTKLEIKR 106
DB 61 SGSGSGTDFLTITSLQPEDFATYCCQSYSTYTFYFGQGTKEIKR 106
RESULT 6
AAG93590
ID AAG93590 standard; protein; 107 AA.
XX AAG93590;
AC AAG93590;
XX 14-SEP-2001 (first entry)
DT Human anti-Rh(D) chain 102 protein sequence.
DE
XX

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX Homo sapiens.
XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-00240274.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX N-PSDB; AAG68647.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Claim 1; Col 43; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAG68615 to AAG68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX Sequence 107 AA;
SQ
Query Match 88.3%; Score 483; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.5e-26;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTTTCARQSIYLYNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTTTCARQSIYLYNWYQOKPGKAPKLLIWSASNLQSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLQFEDFASYCQSYTYLLTYFGSGTKLEIKR 106
DB 62 SGSGSGTDFLTITSLQPEDFATYCCQSYSTYTFYFGQGTKEIKR 107
RESULT 7
ABO27397
ID ABO27397 standard; protein; 107 AA.
XX ABO27397;
AC ABO27397;
XX 12-SEP-2003 (first entry)
DT Anti-Rh(D) chain 102.
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX Homo sapiens.
XX US2003040605-A1.
XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.
 XX 11-OCT-1996; 96US-0028550P.
 XX 27-JUN-1997; 97US-00884045.
 XX 10-APR-1998; 98US-0081380P.
 XX 29-JAN-1999; 99US-00240274.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Siegel DL;
 XX WPI; 2003-512273/48.
 XX N-PSDB; ACD45311.
 XX New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX Claim 4; Page 26; 187pp; English.
 XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents the amino acid sequence of a human anti-Rh(D) chain
 XX Sequence 107 AA;
 SQ Query Match 88.3%; Score 483; DB 6; Length 107;
 Best Local Similarity 87.7%; Pred. No. 3.5e-26;
 Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
 QY 61 SGSGSGTEFTLTISNLQFDPASYCQSYTTLTYFGSGTKLEIKR 106
 Db 62 SGSGSGTDFLTITSSLPQDPATYTCQSYSTLTWFGQGTKEIKR 107
 RESULT 8
 AAG93644
 ID AAG93644 standard; protein; 107 AA.
 AC AAG93644;
 XX 14-SEP-2001 (first entry)
 XX Human anti-Rh(D) antibody clone SH13 protein sequence.
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX Homo sapiens.
 XX USG255455-B1.
 XX 03-JUL-2001.
 XX 29-JAN-1999; 99US-00240274.
 XX 11-OCT-1996; 96US-0028550P.
 XX 27-JUN-1997; 97US-00884045.
 XX 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Siegel DL;
 XX WPI; 2001-388931/41.
 XX N-PSDB; AAH68701.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 XX therapeutic medicine.
 XX Claim 1; Col 68; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 XX the present invention
 XX Sequence 107 AA;
 SQ Query Match 87.8%; Score 480; DB 4; Length 107;
 Best Local Similarity 87.7%; Pred. No. 5.7e-26;
 Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 Db 2 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
 QY 61 SGSGSGTEFTLTISNLQFDPASYCQSYTTLTYFGSGTKLEIKR 106
 Db 62 SGSGSGTDFLTITSSLPQDPATYTCQSYSTLTWFGQGTKEIKR 107
 RESULT 9
 ABO27451
 ID ABO27451 standard; protein; 107 AA.
 AC ABO27451;
 XX 12-SEP-2003 (first entry)
 XX Anti-Rh(D) light chain SH13.
 XX Human; RH(D) binding protein; blood typing; blood product; antibody;
 KW magnetically activated cell sorting.
 XX Homo sapiens.
 XX US2003040605-A1.
 XX 27-FEB-2003.
 XX 04-MAY-2001; 2001US-00848798.
 XX 11-OCT-1996; 96US-0028550P.
 XX 27-JUN-1997; 97US-00884045.
 XX 10-APR-1998; 98US-0081380P.
 XX 29-JAN-1999; 99US-00240274.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Siegel DL;
 XX WPI; 2003-512273/48.
 XX N-PSDB; ACD45365.
 XX New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX Claim 4; Page 50; 187pp; English.
 XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;
Query Match 87.8%; Score 480; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.7e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SGSGSGTFTLTISNLQPEDFASVYCOQSYTTLTYTFSGQTKLEIKR 106
DB 62 SGSGSGTFTLTISNLQPEDFATYVCOQSYSTPTTFGQGTKEIKR 107
RESULT 10
AAR54261
ID AAR54261 standard; protein; 107 AA.
XX
AC AAR54261;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
XX Anti-HIV gp120 immunoglobulin light chain variable region b27.
XX
DE Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX
XX WO9407922-A1.
PN
XX
PD 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
XX
XX 30-SEP-1992; 92US-00954148.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1994-135516/16.
XX
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp41 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Claim 5; Page 190; 248pp; English.
XX
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification

CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAB regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54261
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 107 AA;
Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-25;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SGSGSGTFTLTISNLQPEDFASVYCOQSYTTLTYTFSGQTKLEIKR 106
DB 61 SGSGSGTFTLTISNLQPEDFATYVCOQSYSTPTTFGQGTKEIKR 106
RESULT 11
AAW01284
ID AAW01284 standard; protein; 107 AA.
XX
AC AAW01284;
XX
DT 29-JAN-1997 (first entry)
XX
XX VL region of HIV neutralising MAB, clone b27.
XX
DE Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX
XX WO9602273-A1.
PN
XX
XX 01-FEB-1996.
XX
XX 11-JUL-1995; 95WO-US008743.
XX
XX 18-JUL-1994; 94US-00276852.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 1996-179601/18.
XX
XX Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in passive
PT immuno:therapy and detection of HIV infection.
XX

PS Example; Fig 11; 366pp; English.

CC The sequences given in AA01261-92 represent the light chain variable

CC regions (VL) of a series of monoclonal antibodies (Mab's) which are

CC immunoreactive with HIV glycoprotein gp120 and are capable of

CC neutralising HIV. This sequence represents the sequence of the JK2 gene

CC clone, b27. A Mab containing this VL sequence has the capacity to reduce

CC HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a

CC concentration of less than 700 ng of antibody/ml, and binds mature gp120

CC preferentially over the precursor gp160. The Mab may be used for

CC determining immunocompetence of a human anti-HIV antibody and in the

CC detection of HIV infection

XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;

Best Local Similarity 87.7%; Pred. No. 1.1e-25;

Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

DB 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 60

QY 61 SSGSGGTFTLTISNLQFDPFASYCQOSYTTLYTFGSGTKLEIKR 106

DB 61 SSGSGGTFTLTISLQPEDFATYCCQSYSTPTQTFGQTKLEIKR 106

RESULT 12

AA098245

ID AAY98245 standard; protein; 107 AA.

XX

AC AAY98245;

XX

DT 04-JUL-2000 (first entry)

XX

DE Anti-gp120 antibody light chain variable region from clone B27.

XX

KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;

KW human immunodeficiency virus type 1; HIV-1; infectivity titre;

KW passive immunotherapy; reduce severity; HIV-induced disease;

KW immunocompetence; active immunisation.

XX

OS Homo sapiens.

XX

PN AU9948754-A.

XX

PD 17-FEB-2000.

XX

PF 16-SEP-1999; 99AU-00048754.

XX

PR 16-SEP-1999; 99AU-00048754.

XX

PA (SCRI) SCRIPPS RES INST.

XX

XX Burton DR, Barbas CF, Lerner RA;

PI

XX WPI; 2000-246867/22.

XX

XX Human neutralizing monoclonal antibodies to human immunodeficiency virus

XX (HIV) used for providing passive immunotherapy to HIV are specific for

XX glycoprotein-120.

XX

XX Example 9; Fig 11; 374pp; English.

PS

XX This sequence represents a fragment of the antibodies of the invention.

XX The invention relates to the production of an anti-HIV (human

XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable

XX of reducing an HIV infectivity titre in an in vitro virus infectivity

XX assay by 50% at a concentration of less than 70 ng/ml. The method for the

XX production of the antibody comprises: (a) providing a first

XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence

XX (which does not comprise the sequence represented by AA098206) and a

CC second polynucleotide encoding a light chain immunoglobulin amino acid

CC sequence; (b) inserting the first and second polynucleotide sequences

CC into a host cell; (c) maintaining the host cell in conditions which allow

CC the amino acid sequences encoded by the polynucleotides to be expressed

CC in the host cell; and (d) isolating the antibody comprising the heavy and

CC light chain immunoglobulin amino acid sequences from the host cell. The

CC anti-HIV gp-120 monoclonal antibody is used for providing passive

CC immunotherapy to HIV in a human. They can be administered to high-risk

CC patients to reduce the likelihood and/or severity of HIV-induced disease

CC and to patients who are already HIV-infected. The antibodies are used for

CC neutralising field isolates which provides information about the

CC immunocompetence of an immune response in HIV patients, for detecting HIV

CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for

CC producing anti-idiotypic antibodies which can be used for active

CC immunisation and to screen human monoclonal antibodies to identify those

CC with the same binding specificity and to monitor the course of HIV

CC disease therapy by measuring the changes in concentration of HIV present

CC in the body or in body fluids by immunoassay. The anti-HIV gp-120

CC monoclonal antibodies are encoded by a human polynucleotide sequence and

CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease

CC reduce the problems of significant host immune response to the antibodies

CC associated with monoclonal antibodies of xenogeneic or chimeric

CC derivation

XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;

Best Local Similarity 87.7%; Pred. No. 1.1e-25;

Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

DB 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 60

QY 61 SSGSGGTFTLTISNLQFDPFASYCQOSYTTLYTFGSGTKLEIKR 106

DB 61 SSGSGGTFTLTISLQPEDFATYCCQSYSTPTQTFGQTKLEIKR 106

RESULT 13

AA095136

ID AAY95136 standard; protein; 107 AA.

XX

AC AAY95136;

XX

DT 30-JUN-2000 (first entry)

XX

XX Anti-gp120 antibody light chain variable region from clone B27.

DE

XX Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;

KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;

KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

XX

OS Homo sapiens.

XX

PN AU9948756-A.

XX

PD 17-FEB-2000.

XX

PF 16-SEP-1999; 99AU-00048756.

XX

PR 16-SEP-1999; 99AU-00048756.

XX

PA (SCRI) SCRIPPS RES INST.

XX

XX Burton DR, Barbas CF, Lerner RA;

PI

XX WPI; 2000-293393/26.

XX

XX Novel human monoclonal antibodies which immunoreact with and neutralize

XX human immunodeficiency virus useful for treating HIV infections.

XX

XX Example 9; Fig 11; 366pp; English.

PS

XX The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
XX
SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-25;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
Qy 61 SGSGSGTEFTLTISNQDFASVYCOQSYTYLTTFGSGTKLEIKR 106
Db 61 SGSGSGTDFLTITSSLQPEDFATYQCQSYSTPTQTFGQGTKEIKR 106

RESULT 14
AAG93663
ID AAG93663 standard; protein; 107 AA.
AC AAG93663;
XX
XX 14-SEP-2001 (first entry)
XX Human anti-Rh(D) antibody clone SH49 protein sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX WPI; 2001-388931/41.
XX

DR N-PSDB; AAH68720.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Claim 1; Col 69; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-25;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 61
Qy 61 SGSGSGTEFTLTISNQDFASVYCOQSYTYLTTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLQPEDFATYQCQSYSTPTQTFGQGTKEIKR 107

RESULT 15
AAG93664
ID AAG93664 standard; protein; 107 AA.
XX
AC AAG93664;
XX
XX 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH50 protein sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
XX N-PSDB; AAH68721.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Claim 1; Col 69; 162pp; English.
XX

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:27:40 ; Search time 15.097 Seconds
(without alignments)
675.565 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSYTTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	85.6	108	2 B49047	Ig kappa chain V r
2	465	85.0	108	2 S47182	Ig kappa chain - h
3	465	85.0	127	2 S40367	Ig kappa chain V-J
4	464	84.8	109	2 S31998	Ig kappa chain - h
5	462	84.5	123	2 S40331	Ig kappa chain - h
6	457	83.5	122	2 S40370	Ig kappa chain - h
7	455	83.2	108	2 S44122	Ig kappa chain V r
8	454	83.0	108	2 S31977	Ig kappa chain - h
9	453	82.8	129	1 K1HUWK	Ig kappa chain pre
10	451	82.4	109	2 S31981	Ig kappa chain - h
11	449	82.4	109	2 S31978	Ig kappa chain - h
12	449	82.1	108	1 K1HURD	Ig kappa chain V-I
13	447	81.7	108	2 S19674	Ig kappa chain V r
14	446	81.5	129	2 S40317	Ig kappa chain - h
15	438	80.1	117	2 S46371	Ig kappa chain V-J
16	437.5	80.0	106	2 PC2397	anti-tetanus toxin
17	437	79.9	107	2 S36264	Ig lambda chain V
18	437	79.9	108	1 K1HURU	Ig kappa chain V-I
19	437	79.9	120	2 S46370	Ig kappa chain V-J
20	436	79.7	109	2 S31979	Ig kappa chain - h
21	434	79.3	129	2 S52793	Ig kappa chain var
22	433	79.2	128	2 S46372	Ig kappa chain - h
23	432	79.0	109	2 S31980	Ig kappa chain - h
24	432	79.0	125	2 S40350	Ig kappa chain - h
25	431	78.8	109	2 S31983	Ig kappa chain - h
26	429	78.4	129	2 S52792	Ig kappa chain V r
27	429	78.4	132	2 S40334	Ig kappa chain - h
28	428	78.2	109	2 S32001	Ig kappa chain - h
29	428	78.2	122	2 S40314	Ig kappa chain - h

RESULT 1

B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176844
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 468; DB 2; Length 108;

Best Local Similarity 84.9%; Pred. No. 3.8e-34; Indels 0; Gaps 0;

Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQISITVLNYYQKPGKAPKLLIWSASNLQSGVPSRF 60

Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSVLNYYQKPGKAPKLLIYAASLQSGVPSRF 62

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTTLTYFGSGTKLEIKR 106

Db 63 SGSGSGTFTLTISNLQFEDFATYCCQSYSTPLTFTGGTKVEIKR 108

RESULT 2

S47182

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C;Accession: S47182

R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

A;Description: Cloning and analysis of IGM anti-thyroglobulin autoantibodies from patient

submitted to the EMBL Data Library, June 1994

A;Reference number: S47181

A;Accession: S47182

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-108 <MCI>

A;Cross-references: UNIPARC:UPI00001161E5; EMBL:X79786; NID:G506422; PIDN:CAA56182.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match	85.0%;	Score 465;	DB 2;	Length 108;	
Best Local Similarity	85.8%;	Pred. No. 6.9e-34;			
Matches	91;	Conservative	9;	Mismatches	6; Indels 0; Gaps 0;

Qy	1	ELTQSPSSLASVGD	RVTTTCRAQSI	STYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60
Db	3	ELTQSPSSLASVGD	RVTTTCRAQSI	STYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	62
Qy	61	SGSGSGTEFTLT	ISNLFQFDP	FASYCQOSYTTLYTFGSGTKLEIKR	106
Db	63	SGSGSGTDFLT	ISSLOPED	FATYCCQOSYSTPTTSGQGTREIKR	108

RESULT 3	
S40367	
Ig kappa chain V-J-C region - human	
C;Species: Homo sapiens (man)	
C;Date: 19-May-1994	#sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367	
R;Klein, R.; Jaenichen, R.; Zachau, H.G.	
Eur. J. Immunol. 23, 3248-3271, 1993	
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.	
A;Reference number: S40312; MUID: 94080891; PMID: 8258341	
A;Accession: S40367	
A;Status: preliminary; translation not shown	
A;Molecule type: mRNA	
A;Residues: 1-127 <KLE>	
A;Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: heterotetramer; immunoglobulin	
F;33-107/Domain: immunoglobulin homology <IMM>	

Query Match	85.0%;	Score 465;	DB 2;	Length 127;	
Best Local Similarity	84.0%;	Pred. No. 8.1e-34;			
Matches	89;	Conservative	11;	Mismatches	6; Indels 0; Gaps 0;

Qy	1	ELTQSPSSLASVGD	RVTTTCRAQSI	STYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60
Db	20	QMTQSPSSLASVGD	RVTTTCRAQSI	SNLYNWYQKPGKAPKLLIWSASNLQSGVPSRF	79
Qy	61	SGSGSGTEFTLT	ISNLFQFDP	FASYCQOSYTTLYTFGSGTKLEIKR	106
Db	80	SGSGSGTDFLT	ISSLOPED	FATYCCQOSYNTPTTTFGQGTKEIKR	125

RESULT 4	
S31998	
Ig kappa chain - human (fragment)	
C;Species: Homo sapiens (man)	
C;Date: 06-Feb-1995	#sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31998	
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.	
submitted to the EMBL Data Library, June 1992	
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as	
A;Reference number: S31977	
A;Accession: S31998	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-109 <POR>	
A;Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:938501; PIDN:CAA78790.1; PID	
C;Superfamily: immunoglobulin V region; immunoglobulin homology	
C;Keywords: heterotetramer; immunoglobulin	
F;16-90/Domain: immunoglobulin homology <IMM>	

Query Match	84.8%;	Score 464;	DB 2;	Length 109;	
Best Local Similarity	85.7%;	Pred. No. 8.5e-34;			
Matches	90;	Conservative	9;	Mismatches	6; Indels 0; Gaps 0;

Qy	2	LTQSPSSLASVGD	RVTTTCRAQSI	STYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	61
Db	4	MTQSPSSLASVGD	RVTTTCRAQSI	SNLYNWYQKPGKAPKLLIWSASNLQSGVPSRF	63

Qy	62	GSQSGTEFTLT	ISNLFQFDP	FASYCQOSYTTLYTFGSGTKLEIKR	106
----	----	-------------	-----------	---------------------------	-----

Db 64 GSGSGTDTLTITSSLPEDFATYYCQSYTTLTYTFTGSGTKLEIKR 108

RESULT 5

S40331

Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40331

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40331

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-123 <KLE>

A/Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDN:CAA51148.1; PII:PII

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 462; DB 2; Length 123;

Best Local Similarity 84.8%; Pred. No. 1.4e-33;

Matches 89; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSLSASVGRVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

Db 19 QMTQSPSLSASVGRVTITCRASISISYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 78

Qy 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIK 105

Db 79 GSGSGTDTLTITSSLPEDFATYYCQOSYTPRTFGQGTKEIK 123

RESULT 6

S40370

Ig kappa chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40370

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; MUID:94080891; PMID:8258341

A/Accession: S40370

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-122 <KLE>

A/Cross-references: UNIPARC:UPI0000116178; EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PII:PII

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/30-104/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 457; DB 2; Length 122;

Best Local Similarity 84.9%; Pred. No. 3.9e-33;

Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSLSASVGRVTITCRAROSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60

Db 17 QLTQSPSLSASVGRVTITCRASISITFLHWYQONLKGKAPKLLIYAASNLQSGVPSRF 76

Qy 61 SGSGSGTEFTLTISNLQPEDFASYCQOSYTTLYTFGSGTKLEIKR 106

Db 77 GSGSGTDTLTITSSLPEDFATYYCQOSYTPRTFGQGTKEIKR 122

RESULT 7

S44122

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

A>Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger chain disulfide bonds.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-129/Product: Ig kappa chain V-1 region (Walker) #status predicted <MAT>

F:23-45/Region: framework 1

F:38-112/Domain: immunoglobulin homology <IMM>

F:46-56/Region: complementarity-determining 1

F:57-71/Region: framework 2

F:72-78/Region: complementarity-determining 2

F:79-110/Region: framework 3

F:111-119/Region: complementarity-determining 3

F:120-129/Region: framework 4

F:45-110/Disulfide bonds: #status predicted

	Query Match	82.8%;	Score 453;	DB 1;	Length 129;
	Best Local Similarity	83.8%;	Pred. No. 9,1e-33;		
	Matches	88;	Conservative	10;	Mismatches 7;
				Indels	0;
				Gaps	0;
Qy	1	ELTQSPSSLSASVGDRTVITTCRAQSI	TYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60	
Db	25	QMTQSPSSLSASVGDRTVITTCRAQSI	SNLYNWYQKPGKAPKLLIYAASSLQSGVTSRF	84	
Qy	61	SGSGSGTEFTLTISNLQPEDFASYCQSY	TYLTFTFGSGTKLEIK	105	
Db	85	SGSGSGTDFTLTISLQPEDSATYCCQSY	STLTFTFGQTRLEIK	129	

RESULT 10

S31981

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31981

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL data library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as A:Reference number: S31977

A:Accession: S31981

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: UNIPARC:UPI0000116494; EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID:G38493

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

	Query Match	82.4%;	Score 451;	DB 2;	Length 109;
	Best Local Similarity	82.9%;	Pred. No. 1.2e-32;		
	Matches	87;	Conservative	8;	Mismatches 10;
				Indels	0;
				Gaps	0;
Qy	2	LTQSPSSLSASVGDRTVITTCRAQSI	TYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	61	
Db	4	MTQSPSSLSASVGDRTVITTCRAQSI	RYLNWYQKPGKAPKLLIHGASTLESIGVPSGRFS	63	
Qy	62	SGSGSGTEFTLTISNLQPEDFASYCQSY	TYLTFTFGSGTKLEIKR	106	
Db	64	SGSGSGTDFTLTISLQPEDIATYCCQSY	STFTFTFGQTKLEIKR	108	

RESULT 11

S31978

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31978

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL data library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as A:Reference number: S31977

A:Accession: S31978

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: UNIPARC:UPI0000116494; EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID:G38493

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

submitted to the EMBL Data Library, June 1992

Submitted to the *EMBL* Data Bank, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations associated with the HLA-DQ2.2 allele
A;Reference number: S31977
A;Accession: S31978
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <P>
A;Cross-references: UNIPARC:UPI0000116491; EMBL:Z15074; NID:g38487; PTDN:CAA78793.1; PTDN:CAA78793.2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>
F:16-90/Domain: immunoglobulin homology <IM>

	Query Match	82.4%	Score 451;	DB 2;	Length 109;	
	Best Local Similarity	82.9%;	Pred. No. 1.2e-3;			
	Matches	87;	Conservative	8;	Mismatches 10; Indels	0; Gaps 0;
Qy	2	LTOPSSLSASVGRVTITCRARQSISTYLNWYOQKPGKAPKLIIWSASNLOSGVPRFS	61			
Dd	4	MTQSPSSLSASVGRVTITCRTSQTISRYLNWYOQIFGKAPKLIFAASTLTQTVPSRFG	63			
Qy	62	GSGSGTFTTLTISNLQPEDFASYCQOSYTPLYTFGSGTKLEIKR	106			
Dd	64	GSGSGTFTTLTISLPDDPATYVCQOSTPTPYTFGGTKLEIKR	108			

RESULT 12

K1H0UE
 Ig kappa chain V-I region (Dee) - human (tentative sequence)
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A01865
 R:Milstein, C.P.; Deverson, E.V.
 Biochem. J. 123, 945-958, 1971
 A:Title: The amino acid sequence of a human kappa light chain.
 A:Reference number: A01865; MUID:72053133; PMID:5124396
 A:Accession: A01865
 A:Molecule type: protein
 A:Residues: 1-108 <MIL>
 A:CROSS-references: UNIPROT:P01597; UNIPARC:UPI000012E141
 A:Note: the C region of this chain as the Inv (3) marker
 C:Genetics:
 A:Gene: GDB:IGKV1
 A:CROSS-references: GDB:I36264
 A:Map position: 2p12-2p12
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two identical heavy (kappa) chains disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into la-
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status predicted

Query Match	82.1%	Score	449	DB	1	Length	108
Best Local Similarity	80.2%	Pred. No.	1.7e-32				
Matches	85	Conservative	13	Mismatches	8	Indels	0
						Gaps	0

[illegible]

RESULT 13

```

RESULT 13
SI9674
Ig kappa chain V region (clone alpha-TEL9) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: SI9674
R:Markes, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

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A:Reference number: S19663; MUID:92085276; PMID:17489994
A:Accession: S19674
A:Accession: S19674
A:Molecule type: mRNA
A:Residues: 1-108 <MAR>
A:Cross-references: UNIPARC:UPI0000115F61; EMBL:X61642;
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Suprafamily: heterotetramer; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domains: immunoglobulin homology 1-IMM;

Query Match	81.7%	Score	447;	DB	2;	Length	108;
Best Local Similarity	83.8%	Pred. No.	2.5e-32;				
Matches	88;	Conservative	8;	Mismatches	9;	Indels	0;
Gaps	0;						

Qy	2	LTQSPSLSASVGDVRVTITCRAPQGISISTYLNWYQQKPKAPKLLIWSASNLQSGVPRFS	61
		::: :::	
Db	4	LTQSPSLSASVGDVRVTITCRAPQGISISTYLNWYQQKPKAPKLLIYAASLTQSGVPRFS	63
		::: :::	
Qy	62	GSQSGTEFTLITINLPEDPASYYCQSYTTLVTFGSGTKLEIKR	106
		::: :::	
Db	64	GSQSGTEFTLITINLPEDPATYVYCOOTNSFPPTFGGKTKLEIKR	108
		::: :::	

RESULT 14

RES0011 14
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40317
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40317
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <KLE>
 A:Cross-references: UNIPARC:UPI0000116143; EMBL:X72427; NID:g441322; PIDN:C
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:37-111/Domain: immunoglobulin homology <IMM>

Query Match	81.5%	Score 446;	DB 2;	Length 129;
Best Local Similarity	81.0%;	Pred. No. 3.7e-32;		
Matches	85;	Conservative	11;	Mismatches 9;
				Indels 0;
				Gaps 0;

Qy	1	ELTQSPSSISASVGRVTTTCARQOSISITLYLNWYQOKCKAPKLIATWSASNLQSGVPSRF	60
Db	24	QMTQSPSSLSLTSLGDRVTTTCASQSIGITLYLNWYQOKCKAPKFLITYIGASSLQSGVPSRF	83
Qy	61	SGSGSGSTFTLTISNLQFEDFASYCQQSQYTTLYTFGSGTKLEIK	105
Db	84	SGSGSGSTDTLTISLQPDFAITYCOOTYSTPTPTFGGKTQKVEIK	128

RESULT 15

A63371
 Ig kappa chain V-J region (T24-3) - human (fragment)
 C:Species: Homo sapiens (man)
 C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 R/Accession: S46371; S38645
 R/Bangsmon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(D)J rearrangement
 A/Accession: S46369; M01D:94313975; PMID:8039491
 A/Molecule type: mRNA
 A/Accession: S46371
 A/Residues: 1-117 <BEN>
 A/Cross-references: UNIPARC:UPI00001165A4; EMBL:Z27172; NID:q415959; PIDN:C
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 P:23-97/Domain: immunoglobulin homology <IMM>

Query Match 80.1% Score 438 DB 2: Length 117;

Mon Apr 3 16:31:40 2006

```

Best Local Similarity 80.6%; Pred: No. 1.7e-31;
Matches 87; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

QY 1 ELTQSPSSIASVGDRTVITTCRAGQISTVLYNMYQOKPGKAPKLLIWSASNLQSGVPSRF 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 QMTQSPFTLSASVGDRTVITTCRASRSISTWLAWYQOKPGKAPKLLIYKASTLESQSGVPSRF 69

QY 61 SGSGSGTEFTLLTSLNQLQPEDFASYCQ--SYTTLTYFGSGTKLEIKR 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 SGSGSGTEFTLLTSLQLQDPDFATYICQYNSYPPYTFGQGTKLEIKR 117

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Search completed: April 3, 2006, 14:38:05
Job time : 16.097 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:37 ; Search time 89.6182 Seconds
(without alignments)
834.496 Million cell updates/sec

Title: US-10-027-725A-11
Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGRVTIT.....QQSYTTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	85.4	108	2	Q9UL77 HUMAN
2	465.5	85.1	107	2	Q96SA9 HUMAN
3	453	82.8	129	1	KV1W HUMAN
4	449	82.1	108	1	KV1E HUMAN
5	448.5	82.0	107	2	Q9UL81 HUMAN
6	437	79.9	108	1	KV1H HUMAN
7	433	79.2	236	2	Q6GMX8 HUMAN
8	431	78.8	236	2	Q6GMW1 HUMAN
9	430	78.6	236	2	Q6GMX0 HUMAN
10	428	78.2	236	2	Q6PIH7 HUMAN
11	424	77.5	108	1	KV1N HUMAN
12	423	77.3	234	2	Q7Z473 HUMAN
13	416	76.1	108	1	KV1B HUMAN
14	416	76.1	108	1	KV1O HUMAN
15	414	75.7	108	2	Q9UL70 HUMAN
16	413.5	75.6	107	1	KV1D HUMAN
17	413	75.5	108	2	Q9UL79 HUMAN
18	412	75.3	129	1	KV1X HUMAN
19	411.5	75.2	109	1	KV1T HUMAN
20	411	75.1	108	1	KV1S HUMAN
21	408	74.6	108	1	KV1V HUMAN
22	408	74.6	236	2	Q7Z3Y4 HUMAN
23	407	74.4	108	1	KV1F HUMAN
24	405	74.0	236	2	Q502W4 HUMAN
25	403	73.7	108	1	KV1P HUMAN
26	402	73.5	108	1	KV1A HUMAN
27	402	73.5	108	1	KV1G HUMAN
28	401	73.3	108	1	KV1J HUMAN
29	401	73.3	108	1	KV1I HUMAN
30	401	73.3	234	2	Q5EF66 HUMAN
31	401	73.3	236	2	Q6PIF5 HUMAN

32	399	72.9	108	1	KV1R HUMAN	P01610 homo sapien
33	398	72.8	189	2	Q569I7 HUMAN	Q569I7 homo sapien
34	398	72.8	236	2	Q6GMX9 HUMAN	Q6GMX9 homo sapien
35	397	72.6	244	2	Q65ZC8 HUMAN	Q65ZC8 homo sapien
36	396	72.4	108	1	KV1C HUMAN	P01595 homo sapien
37	395	72.2	108	1	KV1M HUMAN	P01605 homo sapien
38	395	72.2	236	2	Q6PIH4 HUMAN	Q6PIH4 homo sapien
39	394	72.0	240	2	Q65ZC9 HUMAN	Q65ZC9 homo sapien
40	393	71.8	108	1	KV1K HUMAN	P01603 homo sapien
41	394	70.2	108	1	KV1Q HUMAN	P01609 homo sapien
42	384	70.2	108	1	KV5M MOUSE	P01646 mus musculu
43	383	70.0	117	1	KV1J HUMAN	P01602 homo sapien
44	377	68.9	117	1	KV1I HUMAN	P01601 homo sapien
45	375	68.6	108	1	KV5N MOUSE	P01647 mus musculu

ALIGNMENTS

RESULT 1
Q9UL77 HUMAN
ID Q9UL77_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77; HUMAN
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL [2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autoimmune repertoire."
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RX EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSPSP; P01607; 1BWW.
DR SMR; Q9UL77; 1-108.
DR Ensemble; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 85.4%; Score 467; DB 2; Length 108;
Best Local Similarity 84.0%; Pred. No. 4.4e-41;

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Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPNLLIYAASSLQSGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGSGSGTEFTLTISNLFQEDFASYYCQSYTYLYTFGSGTKLEIKR 106
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDTFTLTISLQPEDFATYYCQSYSTSWTFEGGTVKVIKR 108
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
Q96SA9 HUMAN
ID Q96SA9 HUMAN PRELIMINARY; PRT; 107 AA.
AC Q96SA9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98375893; PubMed=9712075;
RA "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis; human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pasqual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with autoantibodies graves use VH and VL gene
RT segments associated with the autoimmune repertoire";
RL Eur. J. Immunol. 22:2231-2236 (1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation";
RL Eur. J. Immunol. 23:391-397 (1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pilling M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype";
RL J. Exp. Med. 174:1639-1652 (1991).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1903706;
RA Blaison G., Kuntz J.L., Pasquali J.L.;
RT "Molecular analysis of V kappa III variable regions of polyclonal
RT rheumatoid factors during rheumatoid arthritis";
RL Eur. J. Immunol. 21:1221-1227 (1991).
DR EMBL; U96396; AAB68785.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; IBMW.
DR SMR; Q96SA9; 1-107.
```

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 85.1%; Score 465.5; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 6.3e-41;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGSGSGTEFTLTISNLFQEDFASYYCQSYTYLYTFGSGTKLEIKR 106
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDTFTLTISLQPEDFATYYCQSYSTLTFGGGTVKVIKR 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
KV1W HUMAN
ID KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006 (1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pasqual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal striational autoantibodies isolated from thymic B
RT lymphocytes of patients with autoantibodies graves use VH and VL gene
RT segments associated with the autoimmune repertoire";
RL Eur. J. Immunol. 22:2231-2236 (1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation";
RL Eur. J. Immunol. 23:391-397 (1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pilling M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype";
RL J. Exp. Med. 174:1639-1652 (1991).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1903706;
RA Blaison G., Kuntz J.L., Pasquali J.L.;
RT "Molecular analysis of V kappa III variable regions of polyclonal
RT rheumatoid factors during rheumatoid arthritis";
RL Eur. J. Immunol. 21:1221-1227 (1991).
DR EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
DR PIR; A01883; KLIHWK.
DR HSSP; P01607; IBMW.
DR SMR; P04431; 23-129.
DR Ensembl; BNSG00000163245; Homo sapiens.
DR GO; GO:0005576; Extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT REGION 23 45 Framework-1.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 119 Complementarity-determining-3.
FT REGION 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129
FT NON_TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;
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Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 1.6e-39;
Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITTCRQSIISTYLNWYQKPGKAPKLLIYAASSLQSGVTSRF 84

QY 61 SGSGSGTFTLTISNLFQEDFASVYCOQSYTTLTFTGSGTKLEIKR 105
DB 85 SGSGSGTFTLTISNLFQEDFASVYCOQSYTTLTFTGSGTKLEIKR 129

RESULT 4
KV1H_HUMAN STANDARD; PRT; 108 AA.
ID KV1H_HUMAN
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-1 region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=72053133; PubMed=5124396;
RX Milstein C.P.; Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain."
RL Biochem. J. 123:945-958 (1971).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR: A01865; KIHUDE.
DR HSP; P01607; 1BW.
DR SMR; P01597; 4-108.
DR GO; GO:000576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT REGION 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 3.4e-39;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
DB 3 ZMTQSPSSLSASVGDRTVITTCRQSIISTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62

QY 61 SGSGSGTFTLTISNLFQEDFASVYCOQSYTTLTFTGSGTKLEIKR 106

DB 63 SGSGSGTFTLTISNLFQEDFATYTCQSYTTLTFTGSGTKLEIKR 108

RESULT 5
Q9UL81_HUMAN
ID Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035033; AAD56269.1; -; mRNA.
DR HSP; P01607; 1BW.
DR SNR; Q9UL81; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 107 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 82.0%; Score 448.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 3.8e-39;
Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRQSIISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRQSIISTYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 62

QY 61 SGSGSGTFTLTISNLFQEDFASVYCOQSYTTLTFTGSGTKLEIKR 106
DB 63 SGSGSGTFTLTISNLFQEDFATYTCQSYTTLTFTGSGTKLEIKR 107

RESULT 6
KV1H_HUMAN STANDARD; PRT; 108 AA.
ID KV1H_HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-1 region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RX Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups."
RL Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----

DR PIR; A01868; KJUHUU.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT REGION 108 108
FT DISULFID 23 88
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 6.2e-38;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRASQISITLYNWKQKPGKAPKLLIWSANLSQGVPSRF 60
DB 3 QMTQSPSSLASVGDRTVITCRASQISITLYNWKQKPGKAPKLLIWSANLSQGVPSRF 62

QY 61 SGSGSGTEFTLTISNLOFEDFASYVCOQSYTYLYTFGSGTKLEIKR 106
DB 63 SGSGSGTDFLTITSSSQPEDFATYVCOQSYTYLYTFGSGTKLEIKR 108

RESULT 7
Q6GMX8_HUMAN
ID Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
TTISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559BF9C9 CRC64;

Query Match 79.2%; Score 433; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 4e-37;
Matches 82; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRASQISITLYNWKQKPGKAPKLLIWSANLSQGVPSRF 60
DB 25 QMTQSPSSLASVGDRTVITCRASQISITLYNWKQKPGKAPKLLIWSANLSQGVPSRF 84

QY 61 SGSGSGTEFTLTISNLOFEDFASYVCOQSYTYLYTFGSGTKLEIKR 106
DB 85 SGSGSGTDFLTITSSSQPEDFATYVCOQSYTYLYTFGSGTKLEIKR 130

RESULT 8
Q6GMW1_HUMAN
ID Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
TTISSUE=Splice;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,


```
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
REMBL; BC073791; AAH73791.1; -; mRNA.
DR SNR; Q6GMW1. 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6GA087AFAC437 CRC64;

Query Match 78.8%; Score 431; DB 2; Length 236;
Best Local Similarity 79.2%; Pred. No. 6.6e-37;
Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVITTCRQSIQSYLYNWYQKPGKAPKLLIWSASLQSGVPSRF 60
Db 25 QMTQSPSLASVGDRTVITTCRQSIQSYLYNWYQKPGKAPKLLIYAASLQSGVPSRF 84

Qy 61 SGSGSGTFTLTISLQPEDFASVYCOQSYTYLTTFGSGTKLEIKR 106
Db 85 SGSGSGTFTLTISLQPEDFATYCYLQDYNYPWTFGGTKVEIKR 130

RESULT 9
Q6GMXO_HUMAN
ID Q6GMXO_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMXO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
REMBL; BC073775; AAH73775.1; -; mRNA.
DR SNR; Q6GMX0. 23-236.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 78.6%; Score 430; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 8.3e-37;
Matches 82; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVITTCRQSIQSYLYNWYQKPGKAPKLLIWSASLQSGVPSRF 60
Db 25 QMTQSPSLASVGDRTVITTCRQSIQSYLYNWYQKPGKAPKLLIYAASLQSGVPSRF 84

Qy 61 SGSGSGTFTLTISLQPEDFASVYCOQSYTYLTTFGSGTKLEIKR 106
Db 85 SGSGSGTFTLTISLQPEDFATYCYCOQSYNPWTFGGTNVEIKR 130

RESULT 10
Q6PIH7_HUMAN
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGC protein.
GN Name=IGC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; IAR2.
DR SMR; Q6P7H7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig CL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8B561106861213F CRC64;

Query Match 78.2%; Score 428; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 1.4e-36;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QLTQSPFLSASVGDRTTTCRASQGISYLAWYQKPGKAPNLLIYAASLTQSGVPSRF 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLPQEDFASYYCOQSYTYLTLYTFSGKTKLEIKR 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SGSGSGTEFTLTISNLPQEDFATYYCOQLNSPPTFGGKTKVLEIKR 130
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
KV1N HUMAN STANDARD; PRT; 108 AA.
AC P01606; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
ON NCBI_TaxID=9606;
RX [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains";
RL Science 169:56-59(1970).
RC -|- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -|- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01872; KIHUOU.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular region; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Framework-2.
FT REGION 35 49 Framework-3.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Complementarity-determining-3.
FT REGION 89 97 Complementarity-determining-4.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11779 MW; 8283D4A24105827E CRC64;

Query Match 77.5%; Score 424; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 1.4e-36;
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQISTYLNWYQKPGKAPKLLIWSANLQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTZSPSSLSASVGBRVTITCRASZTISYLBWYZZKPGKAPBLLIYAASBLHSGVPSRF 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLPQEDFASYYCOQSYTYLTLYTFSGKTKLEIKR 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTEFTLTISNLPZBFATYYCZSYSPPTFGZGTRLEIKR 108
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
Q72473 HUMAN PRELIMINARY; PRT; 234 AA.
ID Q72473; 2003 (Created)
AC Q72473; 2003 (Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGKC protein.
DE Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
ON NCBI_TaxID=9606;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richardson S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;

RG NIH MGC Project;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC056256; AHS6256.1; -, mRNA.
 DR HSSP; P01834; IHEZ.
 DR SNR; Q72473; 22-234.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 2.
 DR PROSITE; PS0290; IG_MHC; UNKNOWN_1.
 KW Immunoglobulin domain
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

 Query Match 77.3%; Score 423; DB 2; Length 234;
 Best Local Similarity 78.1%; Pred. No. 4.5e-36;
 Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

 QY 2 LTQSPSSLSASVGDRTVITCRARQSIITYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 24 MTQSPSFSASTGDRVTITCRASQISGLYAWYQKPGKAPQLLIYAASLTQSGVPSRF 83
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

 QY 62 GSGSGTEFTLTISNLQFDPASYCQSYTTLTYFGSGTKLEIKR 106
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 84 GSASGTDFTLISLCLOSEDFATYCCQYTYPTWTFGGTKVEIKR 128
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

 RESULT 13
 KV1B_HUMAN STANDARD; PRT; 108 AA.
 ID KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-
 Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: The structure of the V region was determined by
 molecular replacement methods using the known structure of the V
 region of the kappa chain REI.
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC PIR; A91653; KIHUAU.
 CC PDB; 1UV5; X-ray; A=1-107.

DR Ensembl; ENSG00000173782; Homo sapiens.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 34
 FT REGION 35 49
 FT REGION 50 56
 FT REGION 57 88
 FT REGION 89 97
 FT REGION 98 107
 FT DISULFID 23 88
 FT NON_TER 108 108
 FT STRAND 4 5
 FT STRAND 10 13
 FT TURN 15 16
 FT TURN 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 44 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6FB9 CRC64;

 Query Match 76.1%; Score 416; DB 1; Length 108;
 Best Local Similarity 76.4%; Pred. No. 1e-35;
 Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

 QY 1 ELTQSPSSLSASVGDRTVITCRARQSIITYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 3 QMTQSPSSLSASVGDRTVITCRASQISGLYAWYQKPGKAPKLLIYDASNLQSGVPSRF 62
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

 QY 61 GSGSGTEFTLTISNLQFDPASYCQSYTTLTYFGSGTKLEIKR 106
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 63 GSGSGGAHFTTISLQPEDFATYCCQYDYLPWTFGGTKVEIKR 108
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

 RESULT 14
 KV10_HUMAN STANDARD; PRT; 108 AA.
 ID KV10_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-I region REI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 kappa-type L-chain, subgroup I (Bence-Jones protein REI); isolation
 and characterization of the tryptic peptides; the complete amino acid

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:36:55 ; Search time 22.6455 Seconds
(without alignments)
386.993 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSSLSASVGRVTIT.....QQSYTTLTYFGSTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/PCRTUS COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	88.5	107	1	US-08-276-852-104
2	484	88.5	107	1	US-08-899-575-104
3	484	88.5	107	1	US-08-899-575-104
4	484	88.5	107	4	PCT-US95-08743-104
5	483	88.3	107	2	US-09-240-274-33
6	483	88.3	107	2	US-09-848-798-33
7	480	87.8	107	2	US-09-240-274-156
8	480	87.8	107	2	US-09-848-798-156
9	476	87.0	107	1	US-08-276-852-105
10	476	87.0	107	1	US-08-899-575-105
11	476	87.0	107	1	US-08-899-575-105
12	476	87.0	107	4	PCT-US95-08743-105
13	475	86.8	107	2	US-09-240-274-175
14	475	86.8	107	2	US-09-848-798-175
15	475	86.8	107	2	US-09-240-274-175
16	475	86.8	107	2	US-09-848-798-175
17	474	86.7	107	2	US-09-240-274-179
18	474	86.7	107	2	US-09-848-798-179
19	473.5	86.6	108	2	US-09-240-274-43
20	473.5	86.6	108	2	US-09-240-274-43
21	473.5	86.6	108	2	US-09-848-798-32
22	473.5	86.6	108	2	US-09-848-798-43
23	473	86.5	107	2	US-09-240-274-37
24	473	86.5	107	2	US-09-848-798-37
25	472.5	86.4	108	2	US-09-240-274-167
26	472.5	86.4	108	2	US-09-848-798-167
27	472	86.3	107	2	US-09-240-274-38

28	472	86.3	107	2	US-09-240-274-39	Sequence 39, Appl
29	472	86.3	107	2	US-09-240-274-162	Sequence 162, App
30	472	86.3	107	2	US-09-848-798-38	Sequence 38, Appl
31	472	86.3	107	2	US-09-848-798-39	Sequence 39, Appl
32	472	86.3	107	2	US-09-848-798-162	Sequence 162, App
33	471	86.1	107	2	US-09-240-274-158	Sequence 158, App
34	471	86.1	107	2	US-09-848-798-158	Sequence 158, App
35	469	85.7	107	2	US-09-240-274-44	Sequence 44, Appl
36	469	85.7	107	2	US-09-848-798-44	Sequence 44, Appl
37	468	85.6	108	1	US-08-379-057-29	Sequence 29, Appl
38	467	85.4	240	2	US-09-192-854-2	Sequence 2, Appl
39	467	85.4	240	2	US-09-511-939-2	Sequence 163, App
40	464.5	84.9	108	2	US-09-240-274-163	Sequence 163, App
41	464.5	84.9	108	2	US-09-848-798-163	Sequence 163, App
42	463	84.6	104	1	US-08-276-852-106	Sequence 106, App
43	463	84.6	104	1	US-08-899-575-106	Sequence 106, App
44	463	84.6	104	1	US-08-899-575-106	Sequence 106, App
45	463	84.6	104	4	PCT-US95-08743-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-104

Query Match 88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASGDRVTTTCRQGISSTYLNWYQQPGKAPKLLIWSASNLQSGVPSRF 60
|||||
|||:
Db 1 ELTQSPSSLASGDRVTTTCRASGISSTYLNWYQQPGKAPKLLIYAASSLQSGVPSRF 60
|||||
|||:

Qy	61	SGSGSGTEFTLTISNLQFEDFASYCQOSYTYLTYPFGSGTKLEIKR	106
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Db	61	SGSGSGTDFTLTISLQPEDFATYYCQOSYSTPYTFGQGTKEIKR	106

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSES: The Scripps Research Institute, Office of
; ADDRESSES: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

```

!
!
! COMPUTER READABLE FORM:
!
! MEDIUM TYPE: Floppy disk
!
! COMPUTER: IBM PC compatible
!
! OPERATING SYSTEM: PC-DOS/MS-DOS
!
! SOFTWARE: PatentIn Release #1.0. Version #1.25
!
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;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/899,575
;; FILING DATE: 24-JUL-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCR1452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEO ID NO: 104:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-575-104

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Query Match 88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels

Qy 1 ELTQSPSSISASVGDRVTTTCRAROSISTYLNWYQQKPGKAPKLLIWSASNTLSQGVPSRF 60

D6 1 ELTQSPSSISASVGDRVTTTCRAROSISSYLNWYQQKPGKAPKLLIYAASLSQGVPSRF 60

Qy 61 S G S G S G T E F T L I S N L Q F E D F A S Y C Q O S Y T T L Y T F G S G T K L E I K R 106
|||||:|||||:|||||:|||||:
Dd 61 S G S G S G T D F T L I S S L O P E D F A T Y Y C Q O S Y S T P Y T F G Q G T K L E I K R 106

RESULT 3
US-08-899-575-104

Sequence 104; Application 03/068333/2
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 1/0
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of
 ADDRESSEE: Patent Counsel
 STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
 STREET: Mail Drop TPC8
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/899,575
 FILING DATE: 24-JUL-1997

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/ FILING DATE: 24 JUL 1994
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/276,852
/ FILING DATE: 18-JUL-1994
/ APPLICATION NUMBER: US 08/178,302
/

```

FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRL452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937

```

;
;
; TELEFAX: 619-554-6312
;
; INFORMATION FOR SEQ ID NO: 104:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 107 amino acids
;
; TYPE: amino acid
;

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;
;      ;
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-899-575-104
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Qy	1	ELTQSPSSLASVGDVRVITTCARQSI	88.7%;	Pred. N
Db	1	ELTQSPSSLASVGDVRVITTCARQSI	94; Conservative	8; Mismatch

QY		61	SCSGGTFTLTISNLQFEDFASYCQOSYTTLTYFGSGTKLEIKR	106
Dd		61	SCSGGTDFTLTISSLOPEDFATYYCQOSYSTPYTFGGTGLEIKR	106

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743

62 SGSGSGTDTLTITSSLOPEDFATYYCOOSYSTLWTFGGTKVEIKR 107

Db 2 ELTQSPSSLSASVGDRVITICRASQSISSYLNWYQQKPKAPKLLIYAASSLRSGVSRF 61

QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTTLTYTFSGKLEIKR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 62 SGSGSGTDFLTLSLQPEDFATYCCQSYSTPTTFTGQGTLEIKR 107
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 8
US-09-848-798-156
; Sequence 156, Application US/09848798
; Patent No. 5858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match 87.8%; Score 480; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 4.5e-16;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 2 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 61
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTTLTYTFSGKLEIKR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 62 SGSGSGTDFLTLSLQPEDFATYCCQSYSTPTTFTGQGTLEIKR 107
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 9
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRL452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-105

Query Match 87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRF 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTTLTYTFSGKLEIKR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 SGSGSGTDFLTLSLQPEDFATYCCQSYSTPTTFTGQGTLEIKR 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163


```
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105

Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ELTQSPSSLASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTYLTFTGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTDFLTITSSLOPEDFATYCCOOSYSTPTQTGGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
US-08-899-575-105
; Sequence 105, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-105

Query Match      87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ELTQSPSSLASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTYLTFTGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTDFLTITSSLOPEDFATYCCOOSYSTPTQTGGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
PCT-US95-08743-105
; Sequence 105, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-105

Query Match      87.0%; Score 476; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ELTQSPSSLASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLOFEDFASYCOOSYTYLTFTGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTDFLTITSSLOPEDFATYCCOOSYSTPTQTGGTKLEIKR 106
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RESULT 13
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRARQSIISYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLASVGDRTVITCRARQSIISYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLOFEDFASYCQSYTTLTYTFSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGSGSGTDFTLTISLQPEDFATYCCQSYSTPTWTFGQGTKEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-09-240-274-176
; Sequence 176, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRARQSIISYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLASVGDRTVITCRARQSIISYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLOFEDFASYCQSYTTLTYTFSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGSGSGTDFTLTISLQPEDFATYCCQSYSTPTWTFGQGTKEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-09-848-798-175
; Sequence 175, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match      86.8%; Score 475; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-35;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITCRARQSIISYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLASVGDRTVITCRARQSIISYLNWYQKPGKAPKLLIYAASLQSGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGSGTEFTLTISNLOFEDFASYCQSYTTLTYTFSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGSGSGTDFTLTISLQPEDFATYCCQSYSTPTWTFGQGTKEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: April 3, 2006, 14:40:32
Job time : 23.6455 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: April 3, 2006, 15:10:27 ; Search time 72.4333 Seconds
(without alignments)
611.458 Million cell updates/sec
Title: US-10-027-725A-11
Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSYTTLTYFGSGTKLEIKR 106
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	547	100.0	106	4	US-10-027-725A-11
2	484	88.5	107	4	Sequence 104, Appl
3	483	88.3	107	3	Sequence 33, Appl
4	480	87.8	107	3	Sequence 156, Appl
5	476	87.0	107	4	Sequence 105, Appl
6	475	86.8	107	3	Sequence 175, Appl
7	475	86.8	107	3	Sequence 176, Appl
8	474	86.7	107	3	Sequence 179, Appl
9	473.5	86.6	108	3	Sequence 32, Appl
10	473.5	86.6	108	3	Sequence 43, Appl
11	473	86.5	107	3	Sequence 37, Appl
12	473	86.5	111	4	Sequence 57, Appl
13	472.5	86.4	108	3	Sequence 167, Appl
14	472	86.3	107	3	Sequence 38, Appl
15	472	86.3	107	3	Sequence 39, Appl
16	472	86.3	107	3	Sequence 162, Appl
17	472	86.3	116	5	Sequence 198, Appl
18	471	86.1	107	3	Sequence 158, Appl
19	470	85.9	157	6	Sequence 27, Appl
20	470	85.9	157	6	Sequence 63, Appl
21	469	85.7	107	3	Sequence 44, Appl
22	468	85.6	108	5	Sequence 209, Appl
23	468	85.6	111	4	Sequence 56, Appl
24	467	85.4	108	4	Sequence 4, Appl
25	467	85.4	108	5	Sequence 90, Appl
26	467	85.4	240	3	Sequence 2, Appl
27	467	85.4	240	3	Sequence 2, Appl

28	467	85.4	240	3	US-09-968-744A-2	Sequence 2, Appl
29	467	85.4	240	3	US-09-968-561A-2	Sequence 2, Appl
30	467	85.4	240	3	US-10-744-774-1	Sequence 1, Appl
31	467	85.4	240	6	US-11-115-682-2	Sequence 2, Appl
32	466	85.2	107	3	US-09-791-153A-67	Sequence 67, Appl
33	466	85.2	108	5	US-10-726-332-214	Sequence 214, App
34	466	85.2	108	5	US-10-805-177-64	Sequence 64, Appl
35	465.5	85.1	107	4	US-10-460-593-9	Sequence 9, Appl
36	465	85.0	107	4	US-10-309-762-89	Sequence 89, Appl
37	465	85.0	108	5	US-10-744-774-15	Sequence 15, Appl
38	465	85.0	108	3	US-09-848-798-163	Sequence 28, Appl
39	464.5	84.9	108	3	US-09-848-798-163	Sequence 163, App
40	464	84.8	108	5	US-10-726-332-18	Sequence 18, Appl
41	463	84.6	104	4	US-10-016-986-106	Sequence 106, App
42	463	84.6	107	4	US-10-309-762-88	Sequence 88, Appl
43	463	84.6	107	5	US-10-727-155-308	Sequence 308, App
44	463	84.6	107	5	US-10-938-353-103	Sequence 103, App
45	462	84.5	108	5	US-10-805-177-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-11
; Sequence 11, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-11

Query Match	100.0%	Score	547	DB	4	Length	106
Best Local Similarity	100.0%	Pred. No.	3.8e-40				
Matches	106	Conservative	0	Mismatches	0	Indels	0
		Gaps	0				
Qy	1	ELTQSPSSLSASVGDRTVITICRARQSTIYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60				
Db	1	ELTQSPSSLSASVGDRTVITICRARQSTIYLNWYQKPGKAPKLLIWSASNLQSGVPSRF	60				
Qy	61	SGSGSGTEFTLTISNLFQDFASYCQSYVTLLYTFGSGTKLEIKR	106				
Db	61	SGSGSGTEFTLTISNLFQDFASYCQSYVTLLYTFGSGTKLEIKR	106				
RESULT 2							
US-10-016-986-104							
; Sequence 104, Application US/10016986							
; Publication No. US20030187247A1							
; GENERAL INFORMATION:							
; APPLICANT: Burton, Dennis R							
; APPLICANT: Barbas, Carlos F							
; APPLICANT: Lerner, Richard A							
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES							
; FILE REFERENCE: 313.2CON1							
; CURRENT APPLICATION NUMBER: US/10/016,986							
; CURRENT FILING DATE: 2001-12-12							
; PRIOR APPLICATION NUMBER: US 09/149,898							
; PRIOR FILING DATE: 1998-09-08							
; PRIOR APPLICATION NUMBER: US 08/899,575							
; PRIOR FILING DATE: 1997-07-24							

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; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      88.5%; Score 484; DB 4; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.2e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 60

QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTYTLTYTFSGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTDFTLTISSLPEDFATYCCQSYSTPTTFTGQGTKEIKR 106

RESULT 3
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-848-798-33

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-34;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTYTLTYTFSGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGSGSGTDFTLTISSLPEDFATYCCQSYSTLTWTFTGQGTKEIKR 107

RESULT 4
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1

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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.6e-34;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 ELTQSPSSLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQSGVPSRF 61

QY 61 SGSGSGTEFTLTISNLFQEDFASYCQSYTYTLTYTFSGTKEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 SGSGSGTDFTLTISSLPEDFATYCCQSYSTPTTFTGQGTKEIKR 107

RESULT 5
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match      87.0%; Score 476; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.8e-34;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 60
QY 61 SGSGSGTEFTLTISNLOPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 61 SGSGSGTDFLTITSSLPEDFATYYCOOSYSTPTQFGGKVEIKR 106

RESULT 6
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 7.1e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLOPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPEDFATYYCOOSYSTPTQFGGKVEIKR 107

RESULT 7
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 86.8%; Score 475; DB 3; Length 107;

Best Local Similarity 85.8%; Pred. No. 7.1e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLOPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPEDFATYYCOOSYSTPTQFGGKVEIKR 107

RESULT 8
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match 86.7%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 8.7e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKPGKAPKLLIYAASLSQSGVPSRF 61
QY 61 SGSGSGTEFTLTISNLOPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTDFLTITSSLPEDFATYYCOOSYSTPTQFGGKVEIKR 107

RESULT 9
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-848-798-32

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US-09-848-798-32
Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.7e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVTTCRASQISISTYLNNWYQQKPGKAPKLLIWSASNLSQGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVTTCRASQISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 61
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QY 61 SGGSGTGTEFTLTISNLOFEDFASYCQOSYTT-LTYFGSGTKLEIKR 106
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Db 62 SGGSGGTDFTLTISSLQPEDFATYYCQOSYSTPPYTFGQGTLEIKR 108
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RESULT 10
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.7e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVTTCRASQISISTYLNNWYQQKPGKAPKLLIWSASNLSQGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVTTCRASQISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGTGTEFTLTISNLOFEDFASYCQOSYTT-LTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SGGSGGTDFTLTISSLQPEDFATYYCQOSYSTPPYTFGQGTLEIKR 108
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RESULT 11
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT

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; SEQ ID NO 167
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-848-798-167

Query Match      86.4%; Score 472.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.3e-33;
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISLQPEDFATYCCQSYSTPTPTFGGKVEIKR 108

RESULT 14
US-09-848-798-38
; Sequence 38, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-848-798-38

Query Match      86.3%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-33;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISLQPEDFATYCCQSYSTPTPTFGGKVEIKR 107

RESULT 15
US-09-848-798-39
; Sequence 39, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
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; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 108
US-09-848-798-39

Query Match      86.3%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-33;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRARQSIISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61

Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTTLYTFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISLQPEDFATYCCQSYSTPTPTFGGKVEIKR 107

Search completed: April 3, 2006, 15:20:22
Job time : 73.4333 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:13:12 ; Search time 9.63636 Seconds
(without alignments)
334.861 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSYTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS5/ptodata/1/pubpaa/US08 NEW_PUB_PEP.*
- 2: /SIDSS5/ptodata/1/pubpaa/US06 NEW_PUB_PEP.*
- 3: /SIDSS5/ptodata/1/pubpaa/US07 NEW_PUB_PEP.*
- 4: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB_PEP.*
- 5: /SIDSS5/ptodata/1/pubpaa/US09 NEW_PUB_PEP.*
- 6: /SIDSS5/ptodata/1/pubpaa/US10 NEW_PUB_PEP.*
- 7: /SIDSS5/ptodata/1/pubpaa/US11 NEW_PUB_PEP.*
- 8: /SIDSS5/ptodata/1/pubpaa/US60 NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	88.3	107	7	US-11-064-174-33
2	480	87.8	107	7	US-11-064-174-156
3	475	86.8	107	7	US-11-064-174-175
4	475	86.8	107	7	US-11-064-174-176
5	474	86.7	107	7	US-11-064-174-179
6	473.5	86.6	108	7	US-11-064-174-32
7	473.5	86.6	108	7	US-11-064-174-43
8	473	86.5	107	7	US-11-064-174-37
9	473	86.5	109	7	US-11-127-932-16
10	473	86.5	109	7	US-11-127-932-17
11	473	86.5	109	7	US-11-127-932-20
12	473	86.5	109	7	US-11-127-903-16
13	473	86.5	109	7	US-11-127-903-17
14	473	86.5	109	7	US-11-127-903-20
15	472.5	86.4	108	7	US-11-064-174-167
16	472	86.3	107	7	US-11-064-174-38
17	472	86.3	107	7	US-11-064-174-39
18	472	86.3	107	7	US-11-064-174-162
19	471	86.1	107	7	US-11-064-174-158
20	469	85.7	107	7	US-11-064-174-44
21	467	85.4	108	6	US-10-925-366A-3
22	467	85.4	108	6	US-10-925-366A-6
23	467	85.4	108	7	US-11-102-512-3
24	467	85.4	108	7	US-11-102-512-6
25	467	85.4	236	7	US-11-086-289-8

26	467	85.4	240	6	US-10-925-366A-219	Sequence 219, App
27	465	85.0	108	7	US-11-127-932-12	Sequence 12, Appl
28	465	85.0	108	7	US-11-127-932-13	Sequence 13, Appl
29	465	85.0	108	7	US-11-127-903-12	Sequence 12, Appl
30	465	85.0	108	7	US-11-127-903-13	Sequence 13, Appl
31	464.5	84.9	108	7	US-11-064-174-163	Sequence 163, App
32	462	84.5	105	7	US-11-155-775-52	Sequence 52, Appl
33	461	84.3	108	6	US-10-771-257-28	Sequence 28, Appl
34	461	84.3	108	6	US-10-834-397-14	Sequence 14, Appl
35	461	84.3	108	6	US-11-127-677-28	Sequence 28, Appl
36	461	84.3	108	7	US-11-049-536-172	Sequence 172, App
37	461	84.3	108	7	US-11-199-739-172	Sequence 168, App
38	459	83.9	107	7	US-11-064-174-168	Sequence 36, Appl
39	459	83.9	108	6	US-10-771-257-36	Sequence 36, Appl
40	459	83.9	108	7	US-11-127-677-36	Sequence 100, App
41	459	83.9	111	7	US-11-049-536-100	Sequence 100, App
42	459	83.9	111	7	US-11-199-739-100	Sequence 30, Appl
43	459	83.9	121	6	US-10-993-543-30	Sequence 36, Appl
44	457	83.5	107	7	US-11-064-174-36	Sequence 71, Appl
45	457	83.5	214	7	US-11-128-900-71	

ALIGNMENTS

RESULT 1

US-11-064-174-33
; Sequence 33, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02

US-11-064-174-33
Query Match 88.3%; Score 483; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 3.4e-35;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITICRAQSIISTYLNWYQQKPGKAPKLLIWAASSLQSGVPSRF 61
Qy 61 SGSGSGTFTLTISNLQFEDFASYCQSYTTLTYFGSGTKLEIKR 106
Db 62 SGSGSGTFTLTISNLQFEDFASYCQSYTTLTYFGSGTKLEIKR 107

RESULT 2

US-11-064-174-156
; Sequence 156, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

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; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-11-064-174-156

Query Match      87.8%; Score 480; DB 7; Length 107;
Best Local Similarity 87.7%; Pred. No. 6.2e-35;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSQISITVLNYYQQKPGKAPKLLIWSASNLQSGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSVLNYYQQKPGKAPKLLIYAASSLSRSGVPSRF 61

QY 61 SSGSGTGTEFTLTISNLFQEDFASYCQSYTYTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGTGDTFTLTSSLPEDFATYYCQSYSTPTPTFGQGTKEIKR 107

RESULT 3
US-11-064-174-175
; Sequence 175, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-064-174-175

Query Match      86.8%; Score 475; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.7e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSQISITVLNYYQQKPGKAPKLLIWSASNLQSGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSVLNYYQQKPGKAPKLLIYAASSLSRSGVPSRF 61

QY 61 SSGSGTGTEFTLTISNLFQEDFASYCQSYTYTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGTGDTFTLTSSLPEDFATYYCQSYSTPTPTFGQGTKEIKR 107

RESULT 4
US-11-064-174-175
; Sequence 175, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-11-064-174-175

Query Match      86.8%; Score 475; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.7e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSQISITVLNYYQQKPGKAPKLLIWSASNLQSGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSVLNYYQQKPGKAPKLLIYAASSLSRSGVPSRF 61

QY 61 SSGSGTGTEFTLTISNLFQEDFASYCQSYTYTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGTGDTFTLTSSLPEDFATYYCQSYSTPTPTFGQGTKEIKR 107

RESULT 5
US-11-064-174-179
; Sequence 179, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-064-174-179

Query Match      86.7%; Score 474; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 2e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSQISITVLNYYQQKPGKAPKLLIWSASNLQSGVPSRF 60
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Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSVLNYYQQKPGKAPKLLIYAASSLSRSGVPSRF 61
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US-11-064-174-176
; Sequence 176, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-11-064-174-176

Query Match      86.8%; Score 475; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.7e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

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Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSVLNYYQQKPGKAPKLLIYAASSLSRSGVPSRF 61

QY 61 SSGSGTGTEFTLTISNLFQEDFASYCQSYTYTLTYFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGTGDTFTLTSSLPEDFATYYCQSYSTPTPTFGQGTKEIKR 107

RESULT 5
US-11-064-174-179
; Sequence 179, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-11-064-174-179

Query Match      86.7%; Score 474; DB 7; Length 107;
Best Local Similarity 85.8%; Pred. No. 2e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSQISITVLNYYQQKPGKAPKLLIWSASNLQSGVPSRF 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITTCRASQSISSVLNYYQQKPGKAPKLLIYAASSLSRSGVPSRF 61
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QY 61 SSGSGTFTLTISNLFQEDFASYCQSYTTLTYFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPEDFATYCCQSYSTPTWTFGGTKVLEIKR 107

RESULT 6
US-11-064-174-32
; Sequence 32, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-11-064-174-32

Query Match 86.6%; Score 473.5; DB 7; Length 108;
Best Local Similarity 87.9%; Pred. No. 2.3e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTTTCRAQSISTVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTTTCRAQSISYSSVLNWKQKPGKAPKLLIYAASLQSGVPSRF 61

RESULT 7
US-11-064-174-43
; Sequence 43, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-11-064-174-43

Query Match 86.6%; Score 473.5; DB 7; Length 108;
Best Local Similarity 87.9%; Pred. No. 2.3e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTTTCRAQSISTVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTTTCRAQSISYSSVLNWKQKPGKAPKLLIYAASLQSGVPSRF 61

RESULT 8
US-11-064-174-37
; Sequence 37, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-11-064-174-37

Query Match 86.5%; Score 473; DB 7; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.5e-34;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRAQSISTVLNWKQKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTTTCRAQSISYSSVLNWKQKPGKAPKLLIYAASLQSGVPSRF 61

RESULT 9
US-11-127-932-16
; Sequence 16, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 109

Query Match 86.8%; Score 473; DB 7; Length 107;
Best Local Similarity 87.9%; Pred. No. 2.3e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 61 SSGSGTFTLTISNLFQEDFASYCQSYTTLTYFGSGTKLEIKR 106
Db 62 SSGSGTDFLTITSSLPEDFATYCCQSYSTPTWTFGGTKVLEIKR 107

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-16

Query Match      86.5%; Score 473; DB 7; Length 109;
Best Local Similarity 85.8%; Pred. No. 2.5e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLSQGVPSRF 60
Db 4 QMTQSPSSLSASVGDRTTTCRASQSIISRYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 63

QY 61 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 106
Db 64 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 109

RESULT 10
US-11-127-932-17
; Sequence 17, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-17

Query Match      86.5%; Score 473; DB 7; Length 109;
Best Local Similarity 85.8%; Pred. No. 2.5e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLSQGVPSRF 60
Db 4 QMTQSPSSLSASVGDRTTTCRASQSIISRYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 63

QY 61 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 106
Db 64 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 109

RESULT 11
US-11-127-932-20
; Sequence 20, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
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; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-20

Query Match      86.5%; Score 473; DB 7; Length 109;
Best Local Similarity 85.8%; Pred. No. 2.5e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLSQGVPSRF 60
Db 4 QMTQSPSSLSASVGDRTTTCRASQSIISRYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 63

QY 61 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 106
Db 64 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 109

RESULT 12
US-11-127-903-16
; Sequence 16, Application US/11127903
; Publication No. US20050288492A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Anti-activated RAS Antibodies
; FILE REFERENCE: 18396/2482
; CURRENT APPLICATION NUMBER: US/11/127,903
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04953
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226728.4
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0316680.8
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB 0226723.5
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226731.8
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-16

Query Match      86.5%; Score 473; DB 7; Length 109;
Best Local Similarity 85.8%; Pred. No. 2.5e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTTTCRARQSIYSTYLNWYQKPGKAPKLLIWSASNLSQGVPSRF 60
Db 4 QMTQSPSSLSASVGDRTTTCRASQSIISRYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 63

QY 61 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 106
Db 64 SGSGSGTFTLTISNLFQDFASYCQSYTYLTLYTSGGKLEIKR 109
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RESULT 13
US-11-127-903-17
; Sequence 17, Application US/11127903
; Publication No. US2005028492A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Anti-activated RAS Antibodies
; FILE REFERENCE: 18396/2482
; CURRENT APPLICATION NUMBER: US/11/127,903
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04953
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226728.4
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0316680.8
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB 0226723.5
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226731.8
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-17

Query Match      86.5%; Score 473; DB 7; Length 109;
Best Local Similarity 85.8%; Pred. No. 2.5e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy      1 ELTQSPSSLSASVGDRTVITTCRARQSIISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      4 QMTQSPSSLSASVGDRTVITTCRASQSIISRYLNWYQQKPGKAPKLLIYAASLQSGVPSRF 63
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      61 SGSGSGTEFTLTISNLPEDFASYCQSYTLYTFGSGTKLEIKR 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      64 SGSGSGTDFLTITSLQPEDFATYCCQSYSTLLTTFGQGTKVEIKR 109
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-11-127-903-20
; Sequence 20, Application US/11127903
; Publication No. US2005028492A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Anti-activated RAS Antibodies
; FILE REFERENCE: 18396/2482
; CURRENT APPLICATION NUMBER: US/11/127,903
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04953
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226728.4
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0316680.8
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB 0226723.5
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226731.8
; PRIOR FILING DATE: 2002-11-15
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; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-20

Query Match      86.5%; Score 473; DB 7; Length 109;
Best Local Similarity 85.8%; Pred. No. 2.5e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy      1 ELTQSPSSLSASVGDRTVITTCRARQSIISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      4 QMTQSPSSLSASVGDRTVITTCRASQSIISRYLNWYQQKPGKAPKLLIYAASLQSGVPSRF 63
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      61 SGSGSGTEFTLTISNLPEDFASYCQSYTLYTFGSGTKLEIKR 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      64 SGSGSGTDFLTITSLQPEDFATYCCQSYSTLLTTFGQGTKVEIKR 109
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-11-064-174-167
; Sequence 167, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 167
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-11-064-174-167

Query Match      86.4%; Score 472.5; DB 7; Length 108;
Best Local Similarity 87.9%; Pred. No. 2.8e-34;
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Qy      1 ELTQSPSSLSASVGDRTVITTCRARQSIISTYLNWYQQKPGKAPKLLIWSASNLQSGVPSRF 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 ELTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPSRF 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      61 SGSGSGTEFTLTISNLPEDFASYCQSYTLYTFGSGTKLEIKR 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 SGSGSGTDFLTITSLQPEDFATYCCQSYSTPPYTFGQGTKLEIKR 108
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: April 3, 2006, 15:21:28
Job time : 10.6364 secs
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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:17:09 ; Search time 92.1879 Seconds
(without alignments)
505.209 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELQSPSSVSASVCDRTVIT.....QQANSPFYTFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	96.0	106	5	Abg30450 Human IgE
2	518	94.4	233	3	Abb03713 Immunoglob
3	518	94.4	233	3	Abb72874 Human AAA
4	493	89.8	107	9	Ady26765 Anti-NGF
5	491	89.4	107	8	Adp22406 Human ant
6	491	89.4	129	9	Adz57711 Germline
7	489	89.1	236	9	Adz57703 Anti-cMet
8	488	88.9	108	9	Aea41079 Germline
9	487	88.7	107	8	Adp22216 Human ant
10	486	88.5	108	9	Aea41087 Germline
11	485	88.3	107	5	Abb07237 Anti-IL-4
12	485	88.3	107	9	Aea08942 Antibody
13	484	88.2	223	6	Abj36940 Anti-CD40
14	483	88.0	129	9	Adz57710 Germline
15	482	87.8	234	7	Adm47073 Mouse ant
16	481	87.6	129	9	Adz57708 Germline
17	479	87.2	107	7	Adp03922 Murine-ex
18	479	87.2	107	7	Adp03994 Murine-ex
19	478	87.1	107	4	Agc65571 Amino aci
20	478	87.1	107	7	Adp03924 Murine-ex
21	478	87.1	107	7	Adp03989 Murine-ex
22	478	87.1	107	7	Adp03921 Murine-ex
23	478	87.1	244	5	Abp45870 Human Bly
24	478	87.1	244	7	Adg96697 Single ch

25	477	86.9	107	9	ADX15508 Human ant
26	477	86.9	107	9	ADX98404 Human ant
27	477	86.9	129	9	ADX98252 Human ant
28	477	86.9	212	8	Adf76324 M16-L 11g
29	475	86.5	236	5	AAU74297 Anti-huma
30	474	86.3	105	5	AAO18424 Anti-GD2
31	474	86.3	107	7	ADK18619 Anti-huma
32	474	86.3	107	7	ADK18794 Anti-huma
33	474	86.3	107	8	ADL25454 Human mAb
34	474	86.3	236	9	ADL25454 Anti-cMet
35	472	86.0	107	7	ADP03920 Murine-ex
36	472	86.0	107	7	ADP03923 Murine-ex
37	471	85.8	236	9	ADZ57695 Anti-cMet
38	470.5	85.7	106	7	ADP03944 Murine-ex
39	469	85.4	129	9	ADZ57726 Anti-cMet
40	468.5	85.3	108	7	ADK18933 Anti-huma
41	468	85.2	234	7	ADE28413 Human ant
42	467	85.1	107	4	AAB72880 Human ant
43	467	85.1	107	8	ADO36490 Human ant
44	467	85.1	107	8	ADO36502 Human ant
45	467	85.1	107	8	ADO36494 Human ant

ALIGNMENTS

RESULT 1
ABG30450
ID ABG30450 standard; protein; 106 AA.
XX
AC ABG30450;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 100 light chain protein.
XX
KW Human, fab; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..21 /note= "FR1 region"
FT Region 22..32 /note= "CDR1 region"
FT Region 33..47 /note= "FR2 region"
FT Region 48..54 /note= "CDR2 protein"
FT Region 55..86 /note= "FR3 region"
FT Misc-difference 65 /note= "Encoded by TCT"
FT Region 87..95 /note= "CDR2 region"
FT Region 96..104 /note= "FR4 region"
FT
FT
WO200253595-A1.
11-JUL-2002.
27-DEC-2001; 2001WO-SE002908.
29-DEC-2000; 2000SE-00004892.
(PHAA) PHARMACIA DIAGNOSTICS AB.
Flicker S, Steinberger P, Kraft D, Valenta R;
WPI; 2002-583604/62.
N-PSDB; ABK89642.

XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgG Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 41; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergen patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC Fab, clone 100 light chain protein of the invention
XX
SQ Sequence 106 AA;

Query Match 96.0%; Score 527; DB 5; Length 106;
Best Local Similarity 97.2%; Pred. No. 7.7e-30;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
QY 61 SSGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
DB 61 SSGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106

RESULT 2
AAB03713
ID AAB03713 standard; protein; 233 AA.
XX
AC AAB03713;
XX
DT 04-OCT-2000 (first entry)
XX
DE Immunoglobulin kappa amino acid sequence fragment.
XX
KW Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
KW abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW immunoglobulin kappa; IgK.
XX
OS Unidentified.
XX
PN US6048704-A.
XX
PD 11-APR-2000.
XX
PF 07-MAR-1997; 97US-00812586.
XX
PR 07-MAR-1996; 96US-0012976P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Tilson MD;
XX
DR WPI; 2000-316895/27.
XX
PT Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
PT disease is purified from human aortic tissue and binds immunoreactively
PT with immunoglobulin.
XX

PS Example 3; Col 29-31; 70pp; English.
XX
CC The present invention relates to an isolated microfibrillar protein of
CC approximately 40kb. The protein is isolated from human aortic tissue and
CC binds immunoreactively with immunoglobulin purified from human abdominal
CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
CC aneurysm-associated antigenic protein (AAP). The protein is capable of
CC forming a disulphide bonded dimer. The protein is immunoreactive with
CC human kappa immunoglobulin. Also included in the invention are
CC recombinantly produced human AAA proteins. AAP shows regions of homology
CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
CC presence of AAA-associated immunoglobulin bound to the human aortic
CC tissue. Antibodies directed against AAP can be used to detect AAA
CC disease. The recombinant protein can be used to induce tolerance to
CC an antigenic AAA protein in the subject e.g. human. This sequence represents
CC an immunoglobulin kappa amino acid sequence. The sequence shares homology
CC with the AAP of the invention, it was used to identify and characterise
CC AAP
XX
SQ Sequence 233 AA;

Query Match 94.4%; Score 518; DB 3; Length 233;
Best Local Similarity 96.2%; Pred. No. 6.6e-29;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
DB 23 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 82
QY 61 SSGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 106
DB 83 SSGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 3
ADB72874
ID ADB72874 standard; protein; 233 AA.
XX
AC ADB72874;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.
XX
KW Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;
KW AAA-associated immunoglobulin 40kDa protein.
XX
OS Homo sapiens.
XX
PN US6537769-B1.
XX
PD 25-MAR-2003.
XX
PF 28-MAR-2000; 2000US-00535832.
XX
PR 07-MAR-1996; 96US-0012976P.
PR 07-MAR-1997; 97US-00812586.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Tilson MD;
XX
DR WPI; 2003-687181/65.
XX
PT Purified protein useful in diagnosing abdominal aortic aneurysm disease
PT in subject, e.g. human, contains specified amino acids.
XX
PS Disclosure; Col 73-74; 67pp; English.
XX
CC The present invention relates to the isolation of a protein approximately
CC 40kDa which is purified from human aortic tissue. The protein is

CC immunoreactive with abdominal aortic aneurysms(AAA)-associated
CC immunoglobulin. The protein is useful for diagnosing AAA disease in a
CC subject, e.g. human, by administering the protein or a composition
CC comprising the protein. The inventive protein is capable of forming a
CC disulphide-bonded dimer of 80 kDa. The present sequence of unknown
CC function is given in the Sequence Listing but is not mentioned elsewhere
CC in the specification.
XX
XX
SQ Sequence 233 AA;

Query Match 94.4%; Score 518; DB 7; Length 233;
Best Local Similarity 96.2%; Pred. No. 6.6e-29;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPKAPKLLIYSASSLSQGVPSRF 60
DB 23 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPKAPKLLIYSASSLSQGVPSRF 82
QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFQGTKEIKR 106
DB 83 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFQGTKEIKR 128

RESULT 4
ADY26765
ID ADY26765 standard; protein; 107 AA.

XX AC ADY26765;
XX
XX 19-MAY-2005 (first entry)
XX
XX Anti-NGF-antibody light chain variable region SEQ ID NO 80.
XX
XX analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
XX neurological disease; NGF; nerve growth factor;
XX light chain variable region.
XX
XX Homo sapiens.

XX WO2005019266-A2.
XX
XX 03-MAR-2005.
XX
XX 15-JUL-2004; 2004WO-US022876.
XX
XX 15-JUL-2003; 2003US-0487431P.
XX (AMGE-) AMGEN INC.
XX
XX Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
XX WPI; 2005-202606/21.
XX
XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful
XX for manufacturing a medicament for treating painful disorders (e.g. acute
XX pain) or conditions associated with increased expression or sensitivity
XX to NGF.
XX
XX Claim 33; SEQ ID NO 80; 190pp; English.

XX The invention describes an isolated human antibody that interacts with or
XX binds specifically to human nerve growth factor (NGF) and neutralize the
XX function of NGF. Also described are: methods of treating a condition
XX caused by increased expression of NGF or increased sensitivity to NGF in
XX a patient; methods for detecting NGF in a biological sample; an NGF
XX specific binding agent comprising any of the 59 amino acid sequences
XX comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
XX specification, and where the binding agent can bind to NGF; a
XX pharmaceutical composition comprising a pharmaceutical carrier and a
XX therapeutic amount of the antibody or binding agent cited above; or a
XX medicament for treating a painful disorder or condition associated with
XX increased expression of NGF or increased sensitivity to NGF, the
XX medicament comprising a pharmaceutical amount of a monoclonal antibody or

CC its immunologically functional immunoglobulin fragment, or pharmaceutical
CC salts of the monoclonal antibody or the fragment, where the monoclonal
CC antibody is at least one of the monoclonal antibody cited above, and a
CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
CC polynucleotide that encodes the above antibody or binding agent; an
CC isolated cell line that produces the above antibody or binding agent; an
CC expression vector comprising the above polynucleotide; and a host cell
CC comprising the nucleic acid or expression vector. The composition
CC (including the antibody) and methods are useful for manufacturing a
CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
CC or pain from trauma or cancer), or a condition associated with increased
CC expression of NGF or increased sensitivity to NGF. This is the amino acid
CC sequence of a human NGF antibody light chain variable region.
XX

SQ Sequence 107 AA;

Query Match 89.8%; Score 493; DB 9; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.9e-27;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOPKAPKLLIYSASSLSQGVPSRF 62
QY 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFQGTKEIKR 105
DB 63 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFQGTKEIKR 107

RESULT 5
ADP22406
ID ADP22406 standard; protein; 107 AA.

XX AC ADP22406;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human anti-TNFA antibody light chain variable region SEQ ID NO:312.
XX
XX human: monoclonal antibody; tumour necrosis factor-alpha; TNFa;
XX anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
XX antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
XX eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
XX prostate cancer; immuno-mediated inflammatory disease;
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
XX septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX Homo sapiens.

XX WO2004050683-A2.
XX
XX 17-JUN-2004.
XX
XX 02-DEC-2003; 2003WO-US038281.
XX
XX 02-DEC-2002; 2002US-0430729P.
XX (ABGE-) ABGENIX INC.
XX Babcock JS, Kang JS, Poord O, Green L, Feng X, Klakamp S;
XX Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
XX Manchulenchko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX WPI; 2004-480601/45.

XX New recombinant human monoclonal antibody that specifically binds to
XX Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX as cancers, or immuno-mediated inflammatory diseases such as rheumatoid

CC cerebral malaria, tumor, and chronic pulmonary inflammatory disease,
CC preferably rheumatoid arthritis. The present sequence represents the
CC germline V kappa L5, J kappa 3 amino acid sequence, which is given in the
CC exemplification of the present invention.

XX Sequence 108 AA;

Query Match 88.9%; Score 488; DB 9; Length 108;
Best Local Similarity 88.7%; Pred. No. 4.3e-27; Indels 0; Gaps 0;
Matches 94; Conservative 7; Mismatches 5;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVPSRF 60

DB 3 QMTQSPSSVSASVGDRTVITCRASQGISWLAHYQHPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGTDFSLTSSQLQFDSATYYCQANSFPYTFGGTKVEIKR 106

DB 63 SSGSGGTDFLTSSQLQPEDFATYYCQANSFPYTFGGTKVDIKR 108

RESULT 9

ID ADP22216 standard; protein; 107 AA.

XX AC ADP22216;

XX DT 09-SEP-2004 (first entry)

XX DE Human anti-TNFA antibody heavy chain variable region SEQ ID NO:122.

XX KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.

XX OS Homo sapiens.

XX XX WO2004050683-A2.

XX XX 17-JUN-2004.

XX PF 02-DEC-2003; 2003WO-US038281.

XX PR 02-DEC-2002; 2002US-0430729P.

XX XX (ABGE-) ABGENIX INC.

XX PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
XX PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
XX PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;

XX XX WPI; 2004-480601/45.

XX DR N-PSDB; ADP22215.

XX XX New recombinant human monoclonal antibody that specifically binds to
XX PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
XX PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
XX PT arthritis.

XX PS Example 10; SEQ ID NO 122; 213pp; English.

XX CC The present invention describes a human monoclonal antibody (I) that
XX CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
XX CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
XX CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFA in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFA in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFA induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFA
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.

XX SQ Sequence 107 AA;

Query Match 88.7%; Score 487; DB 8; Length 107;
Best Local Similarity 89.5%; Pred. No. 5e-27;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVPSRF 60

DB 3 QMTQSPSSVSASVGDRTVITCRASQGISWLAHYQHPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SSGSGYGTDFSLTSSQLQFDSATYYCQANSFPYTFGGTKVEIK 105

DB 63 SSGSGGTDFLTSSQLQPEDFATYYCQANSFPYTFGGTKVEIK 107

RESULT 10

AEA41087

ID AEA41087 standard; protein; 108 AA.

XX AC AEA41087;

XX XX 28-JUL-2005 (first entry)

XX DE Germline V kappa L5, J kappa 4 amino acid sequence SEQ ID NO:117.

XX KW monoclonal antibody; macrophage colony stimulating factor inhibition;
XX KW light chain.

XX OS Unidentified.

XX XX GB2405873-A.

XX XX 16-MAR-2005.

XX XX 09-SEP-2004; 2004GB-00020044.

XX PR 10-SEP-2003; 2003US-0502163P.

XX XX (WARN) WARNER LAMBERT CO LLC.

XX PA (ABGE-) ABGENIX INC.

XX XX Bedian V, Devalaraja MN, Low JE, Mobley JL, Kellermann S;

XX PI Poltz I, Haak-Frendscho M;

XX DR WPI; 2005-216576/23.

Db 25 QMTQSPSSVSGVDRVTITCRASQGISSWLAWYQKPGKAPKLLIYAGSSLSQGVPSRF 84
QY 61 SSGSGYGTDFSLTSSLOFEDSATYVCOQANSFPVTFGQGTKEIKR 106
Db 85 SSGSGFGDTLTSSLOPEDFATYVCOQASSFPRTFGQGTKEIKR 130

RESULT 14

ADZ57710
ID ADZ57710 standard; protein; 129 AA.

AC ADZ57710;

DT 30-JUN-2005 (first entry)

XX Germline antibody L5VK1, Jk3 light chain protein.

XX antibody engineering; cytostatic; vulnery; vasotropic; cardiac;
KW monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;
KW gastrointestinal ulcer; ischemia; transplant rejection;
KW myocardial infarction; reperfusion injury; restenosis; angioplasty;
KW vascular disease; cancer; retinopathy; endometriosis; arthritis;
KW Alzheimers disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;
KW antibody.

XX Homo sapiens.

OS GB2404660-A.

PN 09-FEB-2005.

XX 04-AUG-2004; 2004GB-00017384.

PF 04-AUG-2003; 2003US-0492432P.

PR (PRIZ) PRIZER PROD INC.

PA (ABGE-) ABGENIX INC.

XX Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL;
PI Jia X;

XX WPI; 2005-145169/16.

XX Human monoclonal antibody or antigen-binding portion that specifically
PT binds to c-Met, useful for treating cancer by inhibiting c-Met or for
PT promoting tissue regeneration and wound healing by activating c-Met.

XX Example 2; SEQ ID NO 19; 128pp; English.

XX The invention relates to a human monoclonal antibody (I) or its antigen-
CC binding portion that specifically binds to c-Met, comprises a heavy chain
CC having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is
CC lysine and X4 is threonine, and a light chain having a fully defined
CC sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both
CC chains are without a signal sequence. All the sequences are fully defined
CC in the specification. (I) is useful for the manufacture of a medicament
CC for treating a hyperproliferative disorder in a subject, where the
CC antibody or its portion is a c-Met antagonist. (I) is useful for
CC manufacture of a medicament for promoting wound healing or tissue
CC regeneration in a subject, where the antibody, antigen-binding portion or
CC the composition activates c-Met. (I) which has a c-Met agonist activity
CC is useful in tissue regeneration or wound healing (skin ulcers or gastric
CC ulcers), or treating ischemia associated with kidney transplant
CC rejection, for attenuating toxicity associated with cyclosporin treatment
CC after transplant surgery, for treating myocardial infarction, cardiac
CC ischemia due to reperfusion injury, restenosis after angioplasty or
CC vascular diseases. (I) which has a c-Met antagonist activity is useful
CC for treating cancers of brain, lung, squamous cell, bladder, neck, liver,
CC prostate, etc., proliferative vitreoretinopathy, proliferative diabetic
CC retinopathy, endometriosis, and arthritis, for inhibiting plaque
CC formation in Alzheimer's disease, inhibiting cellular mitogenic
CC responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas.
CC (I) is useful for detecting c-Met in a biological sample in vitro or in

CC vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has
CC selectivity for c-Met that is at least 100 times greater than their
CC selectivity for insulin like growth factor 1 receptor. This sequence
CC corresponds to the amino acid sequence for a germline antibody light
CC chain used in the invention.

XX SQ Sequence 129 AA;

Query Match 88.0%; Score 483; DB 9; Length 129;
Best Local Similarity 88.6%; Pred. No. 1.1e-26;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVTITCRASQGISSWLAWYQKPGKAPKLLIYASASSLSQGVPSRF 60
Db 25 QMTQSPSSVSASVGDRTVTITCRASQGISSWLAWYQKPGKAPKLLIYASASSLSQGVPSRF 84

QY 61 SSGSGYGTDFSLTSSLOFEDSATYVCOQANSFPVTFGQGTKEIK 105

Db 85 SSGSGFGDTLTSSLOPEDFATYVCOQANSFPRTFGQGTKEIK 129

RESULT 15

ADMA7073

ID ADMA7073 standard; protein; 234 AA.

XX AC ADMA7073;

XX 03-JUN-2004 (first entry)

XX Mouse anti-human G-CSF antibody light chain protein.

XX methylotroph yeast; mammalian sugar chain; OCH1; alpha-1;
KW 6-mannosyl transferase; alpha-1; 2-mannosidase;
KW orotidin-5'-phosphate decarboxylase; URA3;

KW phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADE1;

KW imidazole-glycerol-phosphate dehydratase; HIS3;

KW 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;

KW PEP4; YPS1; KTR1; MNN9; AOX; GAPDH; mannosyl transferase;

KW glyceraldehyde 3-phosphate dehydrogenase; mannose glycoprotein.

XX Mus sp.

XX WO2003091431-A1.

XX 06-NOV-2003.

XX 28-APR-2003; 2003WO-JP005464.

XX 26-APR-2002; 2002JP-00127677.

XX (KIRI) KIRIN BEER KK.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX Kobayashi K, Kitagawa Y, Komeda T, Kawashima N, Jigami Y;

XX Chiba Y;

XX WPI; 2003-854401/79.

XX Producing methylotroph yeast that expresses mammalian sugar chains by
XX disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.

XX Example 28; SEQ ID NO 92; 247pp; Japanese.

XX The invention relates to the production of a methylotroph yeast that
CC produces mammalian sugar chains, comprising disrupting the OCH1 gene in
CC the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
CC and expressing the alpha-1,2-mannosidase gene. The specification also
CC includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
CC (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase
CC (ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-
CC isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
CC (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)
CC aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol

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OM protein - protein search, using sw model

Run on: April 3, 2006, 14:27:40 ; Search time 15.097 Seconds
(without alignments)
675.565 Million cell updates/sec

Title: US-10-027-725A-12
Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPYTFGQTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	84.2	117	2 S46376	Ig kappa chain V-J
2	462	84.2	125	2 S40316	Ig kappa chain - h
3	459	83.6	125	2 S40333	Ig kappa chain V-J
4	455	82.9	125	2 S40349	Ig kappa chain V-J
5	454.5	82.8	124	2 S40336	Ig kappa chain V-J
6	454	82.7	130	2 S40368	Ig kappa chain - h
7	451	82.1	128	2 S46372	Ig light chain var
8	451	82.1	131	2 S40352	Ig kappa chain V-J
9	450	82.0	105	2 S36266	Ig lambda chain V
10	447	81.4	127	2 S40367	Ig kappa chain V-J
11	446	81.2	108	2 S19674	Ig kappa chain V r
12	446	81.2	132	2 S38646	Ig kappa chain V r
13	445	81.1	117	2 S46371	Ig kappa chain V-J
14	444	80.9	123	2 S40331	Ig kappa chain - h
15	444	80.9	132	2 S40334	Ig kappa chain - h
16	443	80.7	108	2 B49047	Ig kappa chain - h
17	441	80.3	108	2 S47182	Ig kappa chain - h
18	441	80.3	109	2 S31998	Ig kappa chain V r
19	441	80.3	124	2 S40318	Ig kappa chain V r
20	439.5	80.1	108	2 S30521	Ig kappa chain V r
21	439	80.0	129	2 S40369	Ig kappa chain - h
22	437	79.6	107	2 S36264	Ig lambda chain V
23	435.5	78.3	108	2 S34007	Ig kappa chain V r
24	435	79.2	108	1 K1HUBN	Ig kappa chain V-I
25	434.5	79.1	107	2 S36275	Ig lambda chain V
26	434	79.1	108	1 K1HUWS	Ig kappa chain V-I
27	434	79.1	108	2 S44122	Ig kappa chain pre
28	433	78.9	117	2 S21527	Ig kappa chain V r
29	432	78.7	108	2 S36283	Ig lambda chain V

ALIGNMENTS

RESULT 1

S46376

Ig kappa chain V-J region (T33-14) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C;Accession: S46376; S38649

R;Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement

A;Reference number: S46369; MUID:94313975; PMID:8039491

A;Accession: S46376

A;Molecule type: mRNA

A;Residues: 1-117 <BEN>

A;Cross-references: UNIPARC:UPI0001165A9; EMBL:Z27177; NID:G415969; PIDN:CAA81701.1; PIR

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;25-99/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 117;
Best Local Similarity 84.9%; Pred. No. 2.2e-32;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy	1	ELTQSPSSVSASVGDRTVITCRASQGISSMLAWYQHFGKAPKLLIYSASSLSQSGVPSRF	60
Db	12	QMTQSPSSVSASIGDRVTITCRASQDISMLAWYQKPKAPKLLIYAASSLSQSGVPLRF	71
Qy	61	SGSGYGTDFSLTISLQPEDSATYTCQANSFPYTFGQTKVEIKR	106
Db	72	SGSGSGTDFTLTISLQPEDFATYTCQANSFPRGFGPTKVDIKR	117

RESULT 2

S40316

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40316

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40316

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-125 <KLE>

A;Cross-references: UNIPARC:UPI0000176CAD; EMBL:X72426

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 125;
Best Local Similarity 85.8%; Pred. No. 2.4e-32;

EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <BEN>
A;Cross-references: UNIPARC:UPI0000176CA4; EMBL:Z27173
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 128;
Best Local Similarity 83.8%; Pred. No. 2.1e-31;
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOGKAPKLLIYASASSLQSGVPSRF 61
Db 24 ITQSPSSLSASTGDRVTITTCRASQGISLWAWYQKFGKAPKLLIYAASLTQSGVPSRF 83

Qy 62 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 84 GSGSGTDFLTITISLQFEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 8
S40352
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40352
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40352
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-131 <KLE>
A;Cross-references: UNIPARC:UPI0000116166; EMBL:X72462; NID:9441392; PIDN:CAA51130.1; PID:CAAA43823.1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 131;
Best Local Similarity 83.0%; Pred. No. 2.1e-31;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOGKAPKLLIYASASSLQSGVPSRF 60
Db 23 QMTQSPSSLSASVGNRTVITTCRASQGISLWAWYQKFGKAPKLLIYAASLTQSGVPSRF 82

Qy 61 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 83 GSGSGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 128

RESULT 9
S36266
Ig lambda chain V region (clone alpha-TNF-E1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36266
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36266; MUID:93178448; PMID:7679990
A;Accession: S36266
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-105 <GRI>
A;Cross-references: UNIPARC:UPI0000118DF2; EMBL:Z18840; NID:G33423; PIDN:CAA79292.1; PID:CAAA43823.1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 450; DB 2; Length 105;
Best Local Similarity 85.3%; Pred. No. 2.1e-31;
Matches 87; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOGKAPKLLIYASASSLQSGVPSRF 61
Db 4 LTQSPSSVSASVGDRTVITTCRASQGISLWAWYQKFGKAPKLLIYAASLTQSGVPSRF 63

Qy 62 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVE 103
Db 64 GSGSGTDFLTITISLQFEDSATYCCQANSFPYTFGGTKLE 105

RESULT 10

S40367

Ig kappa chain V-J-C region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40367

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40367

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-127 <KLE>

A;Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 447; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 4.5e-31;
Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOGKAPKLLIYASASSLQSGVPSRF 60
Db 20 QMTQSPSSLSASVGDRTVITTCRASQGISLWAWYQKFGKAPKLLIYAASLTQSGVPSRF 79

Qy 61 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 80 GSGSGTDFLTITISLQFEDSATYCCQANSFPYTFGGTKVEIKR 125

RESULT 11

S19674

Ig kappa chain V region (clone alpha-TEL9) - human

C;Species: Homo sapiens (man)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C;Accession: S19674

R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A;Reference number: S19663; MUID:92085276; PMID:1748994

A;Accession: S19674

A;Molecule type: mRNA

A;Residues: 1-108 <MAR>

A;Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:CAAA43823.1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 4.7e-31;
Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOGKAPKLLIYASASSLQSGVPSRF 61
Db 4 LTQSPSSLSASVGDRTVITTCRASQGISLWAWYQKFGKAPKLLIYAASLTQSGVPSRF 63

```
QY 62 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 64 GSGSGTDFLTILNSLQFEDFATYCCQNTSFPPLTFGGGKLEIKR 108

RESULT 12
S38646
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38646
R;Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <BEN>
A;Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27173; NID:G415961; PIDN:CAA81697.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;40-114/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 132;
Best Local Similarity 82.9%; Pred. No. 5.6e-31;
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPQKAPKLLIYSASSLSQGVPSRF 61
Db 28 IASPSLSASTGDRVTITCRASQGISLWAWYQKQKAPKLLIYAASLTQSGVPSRF 87

QY 62 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 88 GSGSGTDFLTILNSLQFEDFATYCCQNSVYPTTFGGGKLEIKR 132

RESULT 13
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46371; S38645
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46371
A;Molecule type: mRNA
A;Residues: 1-117 <BEN>
A;Cross-references: UNIPARC:UPI00001165A4; EMBL:Z27172; NID:G415959; PIDN:CAA81696.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 445; DB 2; Length 117;
Best Local Similarity 78.7%; Pred. No. 6.1e-31;
Matches 85; Conservative 14; Mismatches 7; Indels 2; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPQKAPKLLIYSASSLSQGVPSRF 60
Db 10 QMTQSPFTLSASVGDRTVITCRASRSISTLWAWYQKQKAPKLLIYKASTLSSQGVPSRF 69

QY 61 GSGYGTDFSLTISLQFEDSATYCCQANSF--PYTFGGGKVEIKR 106
Db 70 GSGSGTDFLTILNSLQFEDFATYCCQNSVYPTTFGGGKLEIKR 117

RESULT 14
S40331
Ig kappa chain - human
C;Species: Homo sapiens (man)
```

```
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>
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```
Query Match 80.9%; Score 444; DB 2; Length 123;
Best Local Similarity 83.8%; Pred. No. 7.8e-31;
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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```
QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPQKAPKLLIYSASSLSQGVPSRF 60
Db 19 QMTQSPFTLSASVGDRTVITCRASQGISLWAWYQKQKAPKLLIYAASLTQSGVPSRF 78

QY 61 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGGKVEIK 105
Db 79 GSGSGTDFLTILNSLQFEDFATYCCQNSVYPTTFGGGKVEIK 123
```

```
RESULT 15
S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: UNIPARC:UPI0000176CA9; EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
```

```
Query Match 80.9%; Score 444; DB 2; Length 132;
Best Local Similarity 80.2%; Pred. No. 8.3e-31;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHQPQKAPKLLIYSASSLSQGVPSRF 60
Db 24 QLTQSPFTLSASIGDRTVITCRASQGISLWAWYQKQKAPKLLIYVASTLQSGVPSRF 83

QY 61 GSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGGKVEIKR 106
Db 84 GSGSGTDFLTILNSLQFEDFATYCCQNSVYPTTFGGGKVEIKR 129
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Search completed: April 3, 2006, 14:38:06
Job time : 15.097 secs
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FCBE14B6559BFC9 CRC64;

Query Match 88.0%; Score 483; DB 2; Length 236;
Best Local Similarity 87.7%; Pred. No. 4.7e-41;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAWYQHQPCKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTVITTCRASQGISWLAWYQHQPCKAPKLLIYAASSLSQGVPSRF 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SSGSGYGTDFSLTSSLOFDSATYYCOQANSFPYTFGQGTKEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SSGSGSGTDFTLTSSLOQDFATYYCOQAHSPFTFGPGTKVDIKR 130
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RESULT 2
Q6GMW1_HUMAN
ID Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AA873791.1; -, mRNA.
DR SMR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.

RESULT 3
Q6PIH7_HUMAN
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -, mRNA.
DR HSSP; P01607; 1A22.
DR SMR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 80.7%; Score 443; DB 2; Length 236;
Best Local Similarity 83.0%; Pred. No. 5.7e-37;
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQSGVPSRF 60
Db 25 QLTQSPSFLSASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYAASTLQSGVPSRF 84

QY 61 SGSGYGTDFSLTISLQFDSATYTCQANSFPYTFGGTKVEIKR 106
Db 85 SGSGGTGFTLTISLQPEDFATYTCQQLNSPPTFGGKVEIKR 130

RESULT 4
Q9UL70 HUMAN
ID Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516816; Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal striational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autoimmune repertoire.";
RT Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174; Wagner S.D., Luzzatto L.;
RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation.";
RT Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; IBBW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 81.1%; Pred. No. 9.9e-37;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYASASSLQSGVPSRF 60
Db 3 QMTQSPSLSASVGDRTVITCRASQGISWLAHYQHOGKAPKLLIYAASTLQSGVPSRF 62

QY 61 SGSGYGTDFSLTISLQFDSATYTCQANSFPYTFGGTKVEIKR 106
Db 63 SGSGGTGFTLTISLQPEDFATYTCQQLNSPPTFGGKVEIKR 108

RESULT 6
KVIV HUMAN
ID KVIV HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-1 region BAN.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Duilet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01878; KIHUBN.
CC DR HSSP; P80362; 1WTL.
CC DR SMR; P04430; 1-108.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC DR SMART; SM00406; IG_v.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin v region.
CC FT REGION 1 23
CC FT REGION 24 34
CC FT REGION 35 49
CC FT REGION 50 56
CC FT REGION 57 88
CC FT REGION 89 97
CC FT REGION 98 107
CC FT REGION 99 108
CC FT DISULFID 23 88
CC FT NON_TER 108 108
CC SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
Query Match 79.2%; Score 435; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 1.6e-36;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QLTQSPSSLSASVGDRTVITCRASQSYNTVAVWFQKPKAPKSLIYDASTLQSGVPSNF 62
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 63 TSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 108
RESULT 7
KV15_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";
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RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01877; KIHUWS.
CC DR HSSP; P80362; 1WTL.
CC DR SMR; P01611; 2-108.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC DR SMART; SM00406; IG_v.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin v region.
CC FT REGION 1 23
CC FT REGION 24 34
CC FT REGION 35 49
CC FT REGION 50 56
CC FT REGION 57 88
CC FT REGION 89 97
CC FT REGION 98 107
CC FT REGION 99 108
CC FT DISULFID 23 88
CC FT NON_TER 108 108
CC SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;
Query Match 79.1%; Score 434; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 2e-36;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTVITCRASQGISLWAWYQHPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITCRASQDISHLAWYQKRSKAPKLLIYSASSLSQGVPSRF 62
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
Db 63 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 108
RESULT 8
Q9UL79_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing V kappa-J kappa recombination after formation of a productive
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RT V kappa-J kappa coding joint." ;
RL Eur. J. Immunol. 22:1561-1565 (1992).
RN [3].
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Iuzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation." ;
RL Eur. J. Immunol. 23:391-397 (1993).
DR ENBL; AF035035; AAD56271.1; -; mRNA.
DR PIR; S23638; S23638.
DR PIR; S30521; S30521.
DR PIR; S34090; S34090.
DR HSP; P01607; IHW.
DR SMK; Q90179; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 79.1%; Score 434; DB 2; Length 108;
Best Local Similarity 81.0%; Pred. No. 2e-36;
Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGRVTTTCRASQGISWLAHYQHPGKAPKLIYSASSLSQGVPSRF 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 MTQSPSLASAGRVTTTCRASQGISWLAHYQHPGKAPKLIYSASSLSQGVPSRF 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 GSGVGTDFSLTISLQSFEDSATYCCQANSFPYTFGGGTVKEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 GSGSGTDFLTITISLQSFEDSATYCCQANSFPYTFGGGTVKEIKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q6GMX9 HUMAN
ID Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

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RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RA NIH MGC Project;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073763; AAH73763.1; -; mRNA.
DR SMR; Q6GMX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;

Query Match 78.1%; Score 429; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 1.5e-35;
Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGRVTTTCRASQGISWLAHYQHPGKAPKLIYSASSLSQGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 QMTQSPSSLSASVGRVTTTCRASQGVSRVLAHYQHPGKAPKLIYSASSLSQGVPSRF 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GSGVGTDFSLTISLQSFEDSATYCCQANSFPYTFGGGTVKEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 GSGSGTDFLTITISLQSFEDSATYCCQANSFPYTFGGGTVKEIKR 130
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q502W4 HUMAN
ID Q502W4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```


RESULT 14																						
ID	Q72473_HUMAN																					
Q72473	Q72473_HUMAN PRELIMINARY; PRT; 234 AA.																					
AC	Q72473																					
DT	01-OCT-2003	(TREMBLrel. 25, Created)																				
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)																				
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)																				
DE	IGKC protein.																					
GN	Name=IGKC;																					
OS	Homo sapiens (Human).																					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;																					
OC	Homo.																					
OX	NCBI_TaxID=9606;																					
OX	[1]																					
RN	NUCLEOTIDE SEQUENCE.																					
RP	TISSUE=Lung;																					
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;																					
RC	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,																					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,																					
RA	Altschul S.P., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,																					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,																					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,																					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,																					
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,																					
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,																					
RA	Posak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,																					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,																					
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,																					
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,																					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,																					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,																					
RA	Rodriguez A.C., Gichwood J., Schmutz J., Myers R.M.,																					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,																					
RA	Scherer A., Schein J.E., Jones S.J.M., Marra M.A.; and																					
RT	"Generation and initial analysis of more than 15,000 full-length human																					
RL	and mouse cDNA sequences."																					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).																					
RN	[2]																					
RP	NUCLEOTIDE SEQUENCE.																					
RC	TISSUE=Lung;																					
RC	NTH MGC Project;																					
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.																					
RL	EMBL; BC065256; AAH56256.1; -; mRNA.																					
DR	HSSP; P01834; 1HEZ.																					
DR	SWR; Q72473; 22-234																					
DR	Ensembl; ENSG00000163245; Homo sapiens.																					
DR	InterPro; IPR007110; Ig-like.																					
DR	InterPro; IPR003597; Ig cl.																					
DR	InterPro; IPR003006; Ig MHC.																					
DR	InterPro; IPR003596; Ig v.																					
DR	Pfam; PF07654; C1-set; I.																					
DR	SMART; SM00406; IG; I.																					
DR	PROSITE; PSS00835; IG LIKE; 2.																					
DR	PROSITE; PS00290; IG MHC; UNKNOWN_1.																					
DR	Immunoglobulin domain.																					
Q72473	SEQUENCE 234 AA; 1A2C259BAB51BC0F CRC64;																					
<table border="0"> <tr> <td>Query Match</td> <td>77.68;</td> <td>Score 426;</td> <td>DB 2;</td> <td>Length 234;</td> </tr> <tr> <td>Best Local Similarity</td> <td>78.1;</td> <td>Pred. No. 3.1e-35;</td> <td></td> <td></td> </tr> <tr> <td>Matches 82;</td> <td>Conservative</td> <td>11;</td> <td>Mismatches 12;</td> <td>Indels 0;</td> </tr> <tr> <td>Gaps</td> <td></td> <td></td> <td></td> <td></td> </tr> </table>			Query Match	77.68;	Score 426;	DB 2;	Length 234;	Best Local Similarity	78.1;	Pred. No. 3.1e-35;			Matches 82;	Conservative	11;	Mismatches 12;	Indels 0;	Gaps				
Query Match	77.68;	Score 426;	DB 2;	Length 234;																		
Best Local Similarity	78.1;	Pred. No. 3.1e-35;																				
Matches 82;	Conservative	11;	Mismatches 12;	Indels 0;																		
Gaps																						
Qy	2 LTQSPSVASVGRVVTTCRASQGISGLAWYHQKPKAPKLITYSASSLSQSGVPSRFS 61																					
Db	24 MTQSPSSFASLTGDRVITTCRASQISGLAWYQQKPKAPQLIIYAASTLQSGVPSRFS 83																					
Qy	62 GSGYGTDFSLTISLQFEDSNTYYCCQANSFPYTFGQTKVEIKR 106																					
Db	84 GSASGTFSLISICLQSEDFAITYCCQYTYTFWTFGQTKVEIKR 128																					

RESULT 15

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Q723Y4 HUMAN
ID Q723Y4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA05332.1; -; mRNA.
DR HSSP; P01834; IHEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWNS.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBPE4ED23084BC6 CRC64;
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Query Match 77.4%; Score 425; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 3.9e-35;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISLAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qy 25 QMTQSPSSLASVGDVTITCRASQDISNLTANFQKPGKAPKSLIYGASSLSQSGVQSKP 84
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qy 61 SGSGYGTDFSLTISLSQFEDSATYCCQANSPFYTFQGTKEIKR 106
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Qy 85 SGSGSGTDFLTISLSQPEDFATYCCQYKSPVTFQGTKEIKR 130
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
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Search completed: April 3, 2006, 14:36:28
Job time : 90.6182 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: April 3, 2006, 14:36:55 ; Search time 22.6455 seconds
(without alignments)
386.993 Million cell updates/sec

Title: US-10-027-725A-12
Perfect score: 549
Sequence: 1 ELTQSPSSVSASVGDRTVTIT.....QQANSPFYTGQTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTRUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Length DB ID	Description
1	518	94.4	233 2 US-08-812-586-45 Sequence 45, Appl
2	518	94.4	233 2 US-09-535-832A-42 Sequence 42, Appl
3	475	86.5	236 2 US-09-859-053-30 Sequence 30, Appl
4	466	84.9	108 2 US-09-920-262A-8 Sequence 8, Appl
5	466	84.9	109 1 US-07-934-373C-3 Sequence 3, Appl
6	466	84.9	109 2 US-08-437-642B-3 Sequence 3, Appl
7	466	84.9	109 2 US-08-146-206C-3 Sequence 3, Appl
8	466	84.9	109 2 US-09-705-686-3 Sequence 3, Appl
9	466	84.9	109 2 US-09-705-392A-3 Sequence 3, Appl
10	466	84.9	109 2 US-09-705-398-3 Sequence 3, Appl
11	466	84.9	109 4 PCT-US93-07832-3 Sequence 4, Appl
12	464.5	84.6	109 2 US-09-798-058-4 Sequence 40, Appl
13	463	84.3	107 2 US-09-240-274-40 Sequence 40, Appl
14	463	84.3	107 2 US-09-848-798-40 Sequence 104, Appl
15	460	83.8	107 1 US-08-276-852-104 Sequence 104, Appl
16	460	83.8	107 1 US-08-899-575-104 Sequence 104, Appl
17	460	83.8	107 4 PCT-US95-08743-104 Sequence 104, Appl
18	460	83.8	108 2 US-08-974-899-3 Sequence 3, Appl
19	460	83.8	108 2 US-09-795-798-3 Sequence 3, Appl
20	460	83.8	108 2 US-08-908-459-12 Sequence 12, Appl
21	460	83.8	108 2 US-08-253-372A-14 Sequence 14, Appl
22	459	83.6	128 1 US-08-468-671-14 Sequence 84, Appl
23	459	83.2	107 1 US-08-276-852-84 Sequence 84, Appl
24	457	83.2	107 1 US-08-899-575-84 Sequence 84, Appl
25	457	83.2	107 1 US-08-899-575-84 Sequence 84, Appl
26	457	83.2	107 1 US-08-899-575-84 Sequence 175, Appl
27	457	83.2	107 2 US-09-240-274-175 Sequence 175, Appl

28	457	83.2	107	2	US-09-240-274-176	Sequence 176, App
29	457	83.2	107	2	US-09-848-798-175	Sequence 175, App
30	457	83.2	107	2	US-09-848-798-176	Sequence 176, App
31	457	83.2	107	4	PCT-US95-08743-84	Sequence 84, Appl
32	456	83.1	107	2	US-09-240-274-156	Sequence 156, App
33	456	83.1	107	2	US-09-848-798-156	Sequence 156, App
34	456	83.1	109	2	US-09-157-370-3	Sequence 3, Appl
35	455	82.9	107	1	US-07-934-373C-18	Sequence 18, Appl
36	455	82.9	107	2	US-08-437-642B-18	Sequence 18, Appl
37	455	82.9	107	2	US-08-146-206C-18	Sequence 18, Appl
38	455	82.9	107	2	US-09-648-067A-14	Sequence 14, Appl
39	455	82.9	107	2	US-09-705-686-18	Sequence 18, Appl
40	455	82.9	107	2	US-09-705-392A-18	Sequence 18, Appl
41	455	82.9	107	2	US-09-705-398-18	Sequence 5, Appl
42	455	82.9	107	2	US-09-602-812A-5	Sequence 18, Appl
43	455	82.9	107	4	PCT-US93-07832-18	Sequence 18, Appl
44	454	82.7	109	2	US-09-025-769B-28	Sequence 28, Appl
45	454	82.7	109	2	US-09-025-769B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-812-586-45
; Sequence 45, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-45

Query Match 94.4%; Score 518; DB 2; Length 233;
Best Local Similarity 96.2%; Pred. No. 3.9e-41;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVSASVGDRTVTITCRASQGISLWAWYCHQPGKAPKLLIYSASSLSQSGVPSRF 60
Db 23 ELTQSPSSVSASVGDRTVTITCRASQGISLWAWYCHQPGKAPKLLIYSASSLSQSGVPSRF 82

QY 61 SGGSGYGTDFSLTSSLOFEDSATYCCOANSFPYTFQGTKEIKR 106
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Db 83 SGGSGGTDFSLTSSLOPEDSATYCCOANSFPYTFQGTKEIKR 128
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RESULT 2
US-09-535-832A-42
; Sequence 42, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-42

Query Match 94.4%; Score 518; DB 2; Length 233;
Best Local Similarity 96.2%; Pred. No. 3.9e-41; Indels 0; Gaps 0;
Matches 102; Conservative 1; Mismatches 3;
QY 1 ELTQSPSSVSASVGDRTTITCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVPSRF 60
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Db 23 ELTQSPSSVSASVGDRTTITCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVPSRF 82
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QY 61 SGGSGYGTDFSLTSSLOFEDSATYCCOANSFPYTFQGTKEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 SGGSGGTDFSLTSSLOPEDSATYCCOANSFPYTFQGTKEIKR 128
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RESULT 3
US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsumari
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match 86.5%; Score 475; DB 2; Length 236;
Best Local Similarity 88.7%; Pred. No. 4.2e-37; Indels 0; Gaps 0;
Matches 94; Conservative 5; Mismatches 7;
QY 1 ELTQSPSSVSASVGDRTTITCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVPSRF 60
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Db 25 QMTQSPSSVSASVGDRTTITCRASQGISRLLAHYQHPGKAPKLLIYVASSLSQGVPSRF 84
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Db 85 SGGSGGTDFTLTSSLOPEDFATYYCOANSFPWTFQGTKEIKR 130
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RESULT 4
US-09-920-262A-8
; Sequence 8, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-8

Query Match 84.9%; Score 466; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.3e-36; Indels 0; Gaps 0;
Matches 90; Conservative 8; Mismatches 8;
QY 1 ELTQSPSSVSASVGDRTTITCRASQGISWLAHYQHPGKAPKLLIYSASSLSQGVPSRF 60
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Db 3 QMTQSPSSVSASVGDRTTITCRASQGISWLAHYQHPGKAPKLLIYVASSLSQGVPSRF 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGGSGYGTDFSLTSSLOFEDSATYCCOANSFPYTFQGTKEIKR 106
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Db 63 SGGSGGTDFTLTSSLOPEDFATYYCOANYPIYTFQGTKEIKR 108
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RESULT 5
US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272

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; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-3

Query Match      84.9%; Score 466; DB 1; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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Db 3 QMTQSPSSLSASVGDRTVITTCRASQDVSSYLAHYQKQKPGKAPKLLIYAASSLSGVPSPRF 62
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QY 61 SGSGYGTDFSLTISLQFEDSATYTCQOANSFPYTFGQGTKEIKR 106
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Db 63 SGSGSGTDFTLTISLQPEDFATYTCQOYNSLPYTFGQGTKEIKR 108
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RESULT 6
US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-3

Query Match      84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHQPQKAPKLLIYASASSLSQSGVPSRF 60
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Db 3 QMTQSPSSLSASVGDRTVITTCRASQDVSSYLAHYQKQKPGKAPKLLIYAASSLSGVPSPRF 62
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QY 61 SGSGYGTDFSLTISLQFEDSATYTCQOANSFPYTFGQGTKEIKR 106
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Db 63 SGSGSGTDFTLTISLQPEDFATYTCQOYNSLPYTFGQGTKEIKR 108
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RESULT 7
US-08-146-206C-3
; Sequence 3, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-3

Query Match      84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHQPQKAPKLLIYASASSLSQSGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLSASVGDRTVITTCRASQDVSSYLAHYQKQKPGKAPKLLIYAASSLSGVPSPRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGSGYGTDFSLTISLQFEDSATYTCQOANSFPYTFGQGTKEIKR 106
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFTLTISLQPEDFATYTCQOYNSLPYTFGQGTKEIKR 108
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RESULT 8
US-09-705-686-3
; Sequence 3, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-Nov-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3
Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHPGKAPKLLIYASLSLQSGVPSRF 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLASVGDRTVITCRASQDVSVSYLAWYQQKPGKAPKLLIYAASLSLQSGVPSRF 62
Qy 61 SGSGYGTDFSLTITSLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
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Db 63 SGSGSGTDFLTITSLQFEDFATYCCQYNSLPYTFGGTKVEIKR 108
RESULT 9
US-09-705-392A-3
; Sequence 3, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-Nov-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-392A-3
Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISWLAHYQHPGKAPKLLIYASLSLQSGVPSRF 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSLASVGDRTVITCRASQDVSVSYLAWYQQKPGKAPKLLIYAASLSLQSGVPSRF 62
Qy 61 SGSGYGTDFSLTITSLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
; |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFLTITSLQFEDFATYCCQYNSLPYTFGGTKVEIKR 108
RESULT 10
US-09-705-398-3
; Sequence 3, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-Nov-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-398-3
Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVSASVGDRTVITICRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITICRASQDVSSYLAHYQKPGKAPKLLIYAASSLSGVPSPRF 62
Qy 61 SGSGYGTDFSLTITSSLOPDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGSGSGTDFLTITSSLOPDSATYCCQANSFPYTFGGTKVEIKR 108
RESULT 11
PCT-US93-07832-3
Sequence 3, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid

TOPOLOGY: linear
PCT-US93-07832-3
Query Match 84.9%; Score 466; DB 4; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
Qy 1 ELTQSPSSVSASVGDRTVITICRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITICRASQDVSSYLAHYQKPGKAPKLLIYAASSLSGVPSPRF 62
Qy 61 SGSGYGTDFSLTITSSLOPDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGSGSGTDFLTITSSLOPDSATYCCQANSFPYTFGGTKVEIKR 108
RESULT 12
US-09-798-058-4
Sequence 4, Application US/09798058
Patent No. 6946546
GENERAL INFORMATION:
APPLICANT: Vaughan, Tristan John
APPLICANT: Wilton, Alison Jane
APPLICANT: Smith, Stephen
APPLICANT: Main, Sarah Helen
TITLE OF INVENTION: Human antibodies against eotaxin and their use
FILE REFERENCE: 84632-000100
CURRENT APPLICATION NUMBER: US/09/798,058
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/187,246
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-058-4
Query Match 84.6%; Score 464.5; DB 2; Length 109;
Best Local Similarity 86.0%; Pred. No. 1.8e-36;
Matches 92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;
Qy 1 ELTQSPSSVSASVGDRTVITICRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITICRASQDVSSYLAHYQKPGKAPKLLIYAASSLSGVPSPRF 62
Qy 61 SGSGYGTDFSLTITSSLOPDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGSGSGTDFLTITSSLOPDSATYCCQANSFPYTFGGTKVEIKR 109
RESULT 13
US-09-240-274-40
Sequence 40, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-40

Query Match      84.3%; Score 463; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.4e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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DB 2 ELTQSPSSLASVGDRTVITTCRASQGISWLAHYQHQPGRKAPKLLIYASASSLSQGVPSRF 61

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSFPYTFQGTKEIKR 106
DB 62 SGSGGTDFTLTSSLOPEDFATYCCQQLNSYPYTFQGTKEIKR 107

RESULT 14
US-09-848-798-40
; Sequence 40. Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I09
US-09-848-798-40

Query Match      84.3%; Score 463; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.4e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYQHQPGRKAPKLLIYASASSLSQGVPSRF 60
DB 2 ELTQSPSSLASVGDRTVITTCRASQGISWLAHYQHQPGRKAPKLLIYASASSLSQGVPSRF 61

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSFPYTFQGTKEIKR 106
DB 62 SGSGGTDFTLTSSLOPEDFATYCCQQLNSYPYTFQGTKEIKR 107

RESULT 15
US-08-276-852-104
; Sequence 104. Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
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;
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 4.6e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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DB 1 ELTQSPSSLASVGDRTVITTCRASQGISWLAHYQHQPGRKAPKLLIYASASSLSQGVPSRF 60

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSFPYTFQGTKEIKR 106
DB 61 SGSGGTDFTLTSSLOPEDFATYCCQSYSTPYTFQGTKEIKR 106

Search completed: April 3, 2006, 14:40:34
Job time : 23.6455 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:10:27 ; Search time 72.4333 Seconds
(without alignments)
611.458 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGDRTIT.....QQANSPPYTFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	100.0	106	4	US-10-027-725A-12
2	493	89.8	107	5	US-10-891-658-80
3	491	89.4	107	5	US-10-727-155-312
4	491	89.4	129	5	US-10-910-901-20
5	489	89.1	236	5	US-10-910-901-12
6	488	88.9	108	5	US-10-938-353-109
7	487	88.7	107	5	US-10-727-155-122
8	486	88.5	108	5	US-10-938-353-117
9	485	88.3	107	5	US-10-982-359-67
10	484	88.2	223	4	US-10-693-629-66
11	483	88.0	129	5	US-10-910-901-19
12	482	87.8	107	4	US-10-309-762-159
13	482	87.8	155	6	US-11-131-648-14
14	482	87.8	155	6	US-11-131-648-37
15	481	87.6	107	4	US-10-292-088-105
16	481	87.6	129	5	US-10-910-901-17
17	479	87.2	107	4	US-10-309-762-62
18	479	87.2	107	4	US-10-309-762-164
19	478	87.1	107	4	US-10-309-762-61
20	478	87.1	107	4	US-10-309-762-64
21	478	87.1	244	3	US-09-880-748-1881
22	478	87.1	244	4	US-10-293-418-1881
23	477	86.9	107	5	US-10-638-265-76
24	477	86.9	107	5	US-10-893-576-177
25	477	86.9	129	5	US-10-893-576-24
26	477	86.9	212	5	US-10-513-725-7
27	475	86.5	236	3	US-09-859-053-30

28	475	86.5	236	4	US-10-800-250-30	Sequence 30, Appl
29	475	86.5	236	4	US-10-625-105-30	Sequence 30, Appl
30	474	86.3	107	4	US-10-041-860-43	Sequence 43, Appl
31	474	86.3	107	4	US-10-041-860-218	Sequence 218, Appl
32	474	86.3	107	4	US-10-665-383-64	Sequence 64, Appl
33	474	86.3	236	5	US-10-910-901-16	Sequence 16, Appl
34	473.5	86.2	106	4	US-10-309-762-84	Sequence 84, Appl
35	472	86.0	107	4	US-10-309-762-60	Sequence 60, Appl
36	472	86.0	107	4	US-10-309-762-63	Sequence 63, Appl
37	471	85.8	236	5	US-10-910-901-4	Sequence 4, Appl
38	468.5	85.3	108	4	US-10-041-860-357	Sequence 357, Appl
39	468	85.2	234	4	US-10-292-088-24	Sequence 24, Appl
40	467	85.1	107	4	US-10-703-714-4	Sequence 4, Appl
41	467	85.1	107	4	US-10-703-714-8	Sequence 8, Appl
42	467	85.1	107	4	US-10-703-714-16	Sequence 16, Appl
43	467	85.1	134	5	US-10-473-287-47	Sequence 47, Appl
44	466	84.9	108	3	US-09-920-262A-8	Sequence 8, Appl
45	466	84.9	108	5	US-10-912-994-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-12
; Sequence 12, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-12

Query Match 100.0%; Score 549; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ELTQSPSSVSASVGDRTITCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF	60
Db	1	ELTQSPSSVSASVGDRTITCRASQGISWLAHYQHOPGKAPKLLIYSASLSQSGVPSRF	60
Qy	61	SGSGYGTDFSLTSSLOFDSATYCCQANSFPYTFGQTKVEIKR	106
Db	61	SGSGYGTDFSLTSSLOFDSATYCCQANSFPYTFGQTKVEIKR	106

RESULT 2

US-10-891-658-80
; Sequence 80, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431

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; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-80

Query Match      89.8%; Score 493; DB 5; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.2e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSFPYTFQGGTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFLTITSSLOPEDFATYCCQANSFPYTFQGGTKVEIK 107

RESULT 3
US-10-727-155-312
; Sequence 312, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaeella Faggoni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ARGENIX.073A
; CURRENT APPLICATION NUMBER: US/10727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-312

Query Match      89.4%; Score 491; DB 5; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.7e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 62

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSFPYTFQGGTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFLTITSSLOPEDFATYCCQANSFPYTFQGGTKVEIK 107

RESULT 4
US-10-910-901-20
; Sequence 20, Application US/10910901
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; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO c-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-20

Query Match      89.4%; Score 491; DB 5; Length 129;
Best Local Similarity 90.5%; Pred. No. 2.1e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 84

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSRPYTFQGGTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SGSGSGTDFLTITSSLOPEDFATYCCQANSFPYTFQGGTKVEIK 129

RESULT 5
US-10-910-901-12
; Sequence 12, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO c-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-12

Query Match      89.1%; Score 489; DB 5; Length 236;
Best Local Similarity 89.6%; Pred. No. 5.6e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASSLSQGVPSRF 84

QY 61 SGSGYGTDFSLTSSLOPEDSATYCCQANSFPYTFQGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SGSGSGTDFLTITSSLOPEDFATYCCQANSFPYTFQGGTKVEIKR 130

RESULT 6
US-10-938-353-109
; Sequence 109, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
```

```

; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 109
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-109

Query Match      88.9%; Score 488; DB 5; Length 108;
Best Local Similarity 88.7%; Pred. No. 3.2e-35;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYAASSLSQSGVPSRF 62

QY 61 SGGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGGSGGTDFLTITSLQPEDFATYCCQANSFPYTFGGTKVDIKR 108

RESULT 7
US-10-727-155-122
; Sequence 122, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaespal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendtscho
; APPLICANT: Palaniawami Rathanaawami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaela Fegioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-122

Query Match      88.7%; Score 487; DB 5; Length 107;
Best Local Similarity 89.5%; Pred. No. 3.9e-35;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYAASSLSQSGVPSRF 62

QY 61 SGGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 105
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Db 63 SGGSGGTDFLTITSLQPEDFATYCCQANSFPYTFGGTKVEIK 107

RESULT 8
US-10-938-353-117
; Sequence 117, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDTSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-117

Query Match      88.5%; Score 486; DB 5; Length 108;
Best Local Similarity 89.6%; Pred. No. 4.8e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYAASSLSQSGVPSRF 62

QY 61 SGGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
Db 63 SGGSGGTDFLTITSLQPEDFATYCCQANSFPYTFGGTKVEIKR 108

RESULT 9
US-10-982-359-67
; Sequence 67, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 63 light chain variable region
US-10-982-359-67

Query Match      88.3%; Score 485; DB 5; Length 107;
Best Local Similarity 88.6%; Pred. No. 5.8e-35;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYSASSLSQSGVPSRF 60
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISLWAWYQHOPGKAPKLLIYAASSLSQSGVPSRF 62
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; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-14

Query Match      87.8%; Score 482; DB 6; Length 155;
Best Local Similarity 89.6%; Pred. No. 1.5e-34;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHQPGRKAPKLLIYASASSLSQSGVPSRF 60
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Db 1 QLTQSPSSVSASVGDRTVITCRASQGISSWLAWYQKPGKAPKLLIYTASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SGSGYGTDFSLTSSLOPESATYCCQANSFPYTFGGTKVEIKR 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTDFLTITSSLOPEDFATYCCQAYSFPRTFGGQTKVEIKR 106
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RESULT 14
US-11-131-648-37
; Sequence 37, Application US/11131648
; Publication No. US20050221400A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Jakobovits, Aya
; APPLICANT: Xiao-Chi, Jia
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Shao, Hui
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
; FILE REFERENCE: 51158-20088.20
; CURRENT APPLICATION NUMBER: US/11/131,648
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/616,381
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: 60/617,881
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/621,310
; PRIOR FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/633,077
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: 10/857,484
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/475,064
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-131-648-37

Query Match      87.8%; Score 482; DB 6; Length 155;
Best Local Similarity 89.6%; Pred. No. 1.5e-34;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHQPGRKAPKLLIYASASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QLTQSPSSVSASVGDRTVITCRASQGISSWLAWYQKPGKAPKLLIYTASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SGSGYGTDFSLTSSLOPESATYCCQANSFPYTFGGTKVEIKR 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGSGSGTDFLTITSSLOPEDFATYCCQAYSFPRTFGGQTKVEIKR 106
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 61 SGSGSGTDFLTITSSLOPEDFATYCCQAYSFPRTFGGQTKVEIKR 106

RESULT 15
US-10-292-088-105
; Sequence 105, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-105

Query Match      87.6%; Score 481; DB 4; Length 107;
Best Local Similarity 89.5%; Pred. No. 1.3e-34;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTVITCRASQGISSWLAWYQHQPGRKAPKLLIYASASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITCRASQGISSWLAWYQKPGKAPKLLIYAASSLSQSGVPSRF 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 SGSGYGTDFSLTSSLOPESATYCCQANSFPYTFGGTKVEIK 105
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFLTITSSLOPEDFATYCCQANSFPLTGGGQTKVEIK 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Job time : 73.4333 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 15:13:12 ; Search time 9.63636 Seconds
(without alignments)
334.861 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSASVGDRTVTIT.....QQANSFPYTFGQTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
- 2: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
- 3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB_PEP.*
- 4: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 5: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB_PEP.*
- 6: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
- 7: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB_PEP.*
- 8: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499	90.9	107	7	US-11-051-453-4
2	499	90.9	129	7	US-11-051-453-43
3	490	89.3	107	7	US-11-051-453-32
4	490	89.3	129	7	US-11-051-453-46
5	478	87.1	244	7	US-11-054-515-1881
6	478	87.1	244	7	US-11-266-444-1881
7	477	86.9	107	6	US-10-956-008-76
8	468	85.2	107	7	US-11-051-453-33
9	468	85.2	129	7	US-11-051-453-47
10	465	84.7	107	7	US-11-051-453-30
11	465	84.7	129	7	US-11-051-453-44
12	464	84.5	107	7	US-11-051-453-34
13	464	84.5	129	7	US-11-051-453-48
14	463	84.3	107	7	US-11-064-174-40
15	462	84.2	234	7	US-11-041-095-25
16	462	84.2	239	7	US-11-041-095-19
17	462	84.2	290	7	US-11-041-095-13
18	460	83.8	108	6	US-10-665-658-3
19	460	83.8	108	7	US-11-120-338-3
20	460	83.8	108	7	US-11-143-077-3
21	460	83.8	108	7	US-11-190-364-3
22	460	83.8	108	7	US-11-147-780-3
23	460	83.8	108	7	US-11-143-386-3
24	460	83.8	108	7	US-11-187-364-3
25	460	83.8	109	6	US-10-981-356A-5

26	450	83.8	109	7	US-11-096-046-5	Sequence 5, Appli
27	458	83.4	108	6	US-10-771-257-77	Sequence 77, Appl
28	458	83.4	108	7	US-11-127-677-75	Sequence 75, Appl
29	458	83.4	108	7	US-11-049-536-228	Sequence 228, App
30	458	83.4	108	7	US-11-199-739-228	Sequence 228, App
31	457	83.2	107	7	US-11-064-174-175	Sequence 175, App
32	457	83.2	107	7	US-11-064-174-176	Sequence 176, App
33	456	83.1	107	7	US-11-064-174-156	Sequence 156, App
34	455	82.9	107	7	US-11-154-337-5	Sequence 5, Appli
35	455	82.9	107	7	US-11-182-908-5	Sequence 5, Appli
36	455	82.9	107	7	US-11-102-120-5	Sequence 5, Appli
37	455	82.9	107	7	US-11-223-361-5	Sequence 3, Appli
38	455	82.9	108	7	US-11-106-820-3	Sequence 14, Appl
39	454	82.7	107	6	US-10-850-635-14	Sequence 18, Appl
40	454	82.7	107	6	US-10-925-366A-187	Sequence 187, App
41	454	82.7	108	6	US-10-834-397-28	Sequence 28, Appl
42	454	82.7	109	6	US-10-834-397-43	Sequence 43, Appl
43	454	82.7	109	6	US-11-054-515-82	Sequence 82, Appl
44	454	82.7	244	7	US-11-054-515-261	Sequence 261, App
45	454	82.7	244	7	US-11-054-515-261	Sequence 261, App

ALIGNMENTS

RESULT 1
US-11-051-453-4
; Sequence 4, Application US/11051453
; Publication NO. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-PEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: US8 THEREOF
; FILE REFERENCE: WJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-4

Query Match 90.9%; Score 499; DB 7; Length 107;
Best Local Similarity 91.4%; Pred. No. 1.8e-35;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ELTQSPSSVSASVGDRTVTITCRASQGISSSWLAWYQHQPFGKAPKLLIYASASSLQSGVPSRF	60
Db	3	QMTQSPSSVSASVGDRTVTITCRASQGISSSWLAWYQHQPFGKAPKLLIYASASSLQSGVPSRF	62
Qy	61	SGSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGQTKVEIK	105
Db	63	SGSGYGTDFSLTISLQFEDSATYTCQANSFPYTFGQTKVEIK	107

RESULT 2
US-11-051-453-43
; Sequence 43, Application US/11051453

```
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 43
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-051-453-43

Query Match          90.9%; Score 499; DB 7; Length 129;
Best Local Similarity 91.4%; Pred. No. 2.1e-35;
Matches 96; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 84

QY 61 SSGSGYGTDFSLTISLQFEDSATYYCOQANSFPYTFGGTKVEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SSGSGGDTFTLTISLQPEDFATYYCOQANSFPWTFGGTKVEIK 129

RESULT 3
US-11-051-453-32
; Sequence 32, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-051-453-32
```

```
Query Match          89.3%; Score 490; DB 7; Length 107;
Best Local Similarity 89.5%; Pred. No. 1e-34;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 62

QY 61 SSGSGYGTDFSLTISLQFEDSATYYCOQANSFPYTFGGTKVEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SSGSGGDTFTLTISLQPEDFATYYCOQANSFPWTFGGTKVEIK 107

RESULT 4
US-11-051-453-46
; Sequence 46, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 46
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-051-453-46

Query Match          89.3%; Score 490; DB 7; Length 129;
Best Local Similarity 89.5%; Pred. No. 1.2e-34;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASASSLSQSGVPSRF 84

QY 61 SSGSGYGTDFSLTISLQFEDSATYYCOQANSFPYTFGGTKVEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SSGSGGDTFTLTISLQPEDFATYYCOQANSFPWTFGGTKVEIK 129

RESULT 5
US-11-054-515-1881
; Sequence 1881, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
```

```

DB      140 MTQSPSTLSASVGDRTVTITCRASQGSISSWLAWTQQKPGKAPKLLIYAASSLQSGVPSRF 199
QY      62 GSGYGTFDSLTSSLOFESATYYCOQANSFPYTFGGTKVEIKR 106
        |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      200 GSGSGTDFTLTISSLQPEDFATYYCOQANSFPLTFGGTKVEIKR 244

RESULT 7
US-10-956-008-76
; Sequence 76, Application US/10956008
; Publication No. US20060062783A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; APPLICANT: Bell, Gregory
; TITLE OF INVENTION: ANTIBODIES AGAINST PARATHYROID HORMONE
; FILE REFERENCE: AGENIX.092CPI
; CURRENT APPLICATION NUMBER: US/10/956,008
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 10/638,265
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-008-76

Query Match      86.9%; Score 477; DB 6; Length 107;
Best Local Similarity 87.6%; Pred.No. 1.2e-33;
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0

QY      1 ELTQSPSSVSASVGDRVTITCRASQGSISSWLAWTQHQPGRKAPKLLIYSASSLQSGVPSRF 60
        :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      3 QMTQSPSSVSASVGDRVTITCRASQGSISSWLAWTQKPGKAPKLLIYAASSLQSGVPSRF 62

QY      61 SGSGYGTFDSLTISSLQFESATYYCOQANSFPYTFGGTKVEIK 105
        |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      63 SGSGSGTDFTLTISSLQPEDFATYYCOQANSFPYTFGGTKVDIK 107

RESULT 8
US-11-051-453-33
; Sequence 33, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BAECKOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOURINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJI-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-11-051-453-33

Query Match 85.2%; Score 468; DB 7; Length 107;
Best Local Similarity 86.7%; Pred. No. 7e-33; 7; Mismatches 0; Gaps 0;
Matches 91; Conservative 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTTTCRASQGISLWAWYQHOPKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTTTCRASQGISLWAWYQKPEKAPKSLIYAASSLSQSGVPSRF 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFLTSSLOPEDFATYCCQYNSYPWTFQGTKEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9

US-11-051-453-47
; Sequence 47, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; FILE REFERENCE: MJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 47
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-47

Query Match 85.2%; Score 468; DB 7; Length 129;
Best Local Similarity 86.7%; Pred. No. 8.2e-33; 7; Mismatches 0; Gaps 0;
Matches 91; Conservative 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTTTCRASQGISLWAWYQHOPKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTTTCRASQGISLWAWYQKPEKAPKSLIYAASSLSQSGVPSRF 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 85 SGSGSGTDFLTSSLOPEDFATYCCQYNSYPWTFQGTKEIK 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10

US-11-051-453-30
; Sequence 30, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH

; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; FILE REFERENCE: MJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 30
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-30

Query Match 84.7%; Score 465; DB 7; Length 107;
Best Local Similarity 85.7%; Pred. No. 1.2e-32; 8; Mismatches 7; Indels 0; Gaps 0;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTTTCRASQGISLWAWYQHOPKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QMTQSPSSVSASVGDRTTTCRASQGISLWAWYQKPEKAPKSLIYAASSLSQSGVPSRF 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 SGSGSGTDFLTSSLOPEDFATYCCQYNSYPWTFQGTKEIK 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11

US-11-051-453-44
; Sequence 44, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; FILE REFERENCE: MJ1-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 44
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-44

Query Match 84.7%; Score 465; DB 7; Length 129;
Best Local Similarity 85.7%; Pred. No. 1.5e-32; 8; Mismatches 7; Indels 0; Gaps 0;
Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGDRTTTCRASQGISLWAWYQHOPKAPKLLIYSASSLSQSGVPSRF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 25 QMTQSPSSVSASVGDRTTTCRASQGISLWAWYQKPEKAPKSLIYAASSLSQSGVPSRF 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SGSGYGTDFSLTSSLOFEDSATYCCQANSFPYTFQGTKEIK 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-11-051-453-48
US-11-051-453-48
Sequence 48, Application US/11051453
Publication No. US20050287150A1
GENERAL INFORMATION:
APPLICANT: AMEROSINO, DONNA
APPLICANT: BABCOCK, GREGORY J.
APPLICANT: BROERING, THERESA
APPLICANT: GRAZIANO, ROBERT
APPLICANT: HERNANDEZ, HECTOR JAVIER
APPLICANT: LOWY, ISRAEL
APPLICANT: MANDELL, ROBERT
APPLICANT: MOLRINE, DEBORAH
APPLICANT: THOMAS, JR., WILLIAM D.
APPLICANT: ZHANG, HUI-FEN
TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: WJ1-001
CURRENT APPLICATION NUMBER: US/11/051,453
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,357
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 60/613,854
PRIOR FILING DATE: 2004-09-28

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein of the TAKA signal peptide sequence from
; OTHER INFORMATION: alpha-amylase from Aspergillus oryzae and a kappa light chain
; OTHER INFORMATION: from Homo sapiens without its native signal peptide
US-11-041-095-25
```

```
Query Match      84.2%; Score 462; DB 7; Length 234;
Best Local Similarity 84.9%; Pred. No. 4.3e-32;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSASVGDRTTTCRASQGISWLAWYQHQPQKAPKLLIYSASSLSQSGVPSRF 60
Db 23 QMTQSPSSLASVGDRTTTCRASQGISWLAWYQHQPQKAPKLLIYSASSLSQSGVPSRF 82

Qy 61 SGSGYGTDFSLTISLQFDSATYYCQANSPYTFQGQTKVEIKR 106
Db 83 SGSGYGTDFSLTISLQFDSATYYCQANSPYTFQGQTKVEIKR 128
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Search completed: April 3, 2006, 15:21:30
Job time : 10.6364 secs